

1/73

FIG. 1A

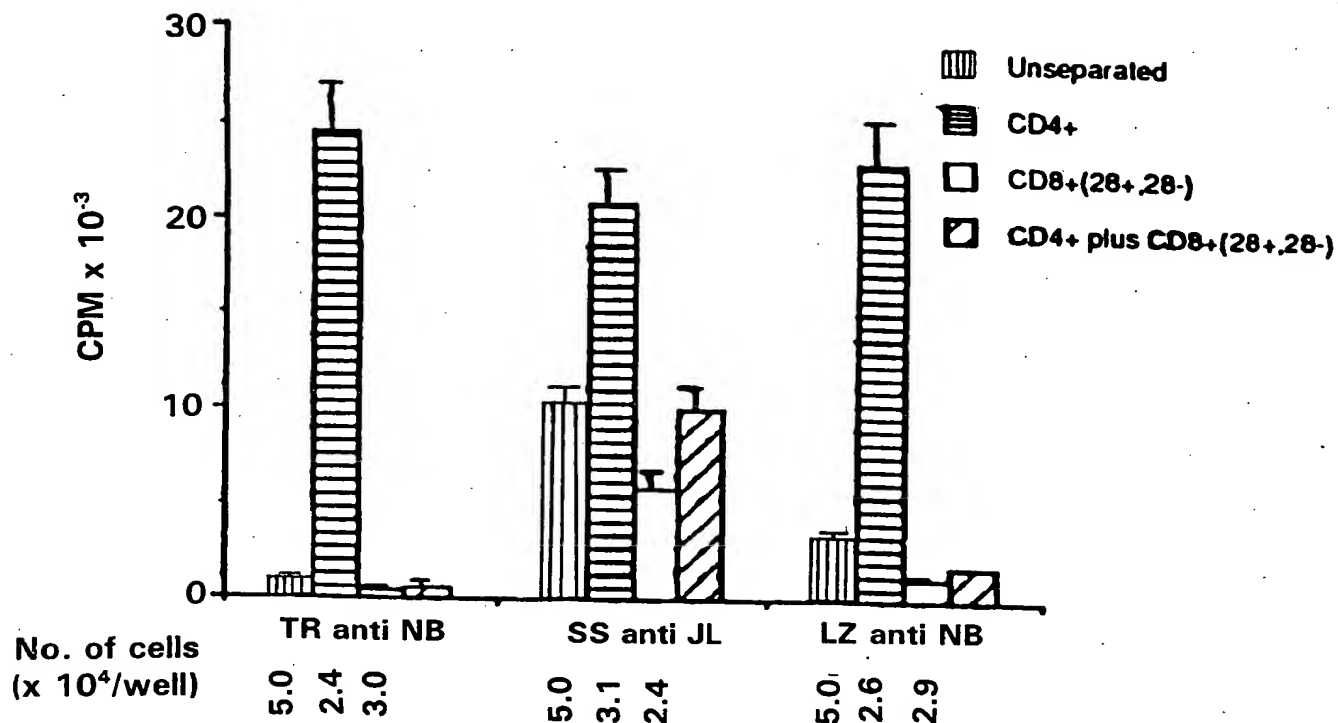
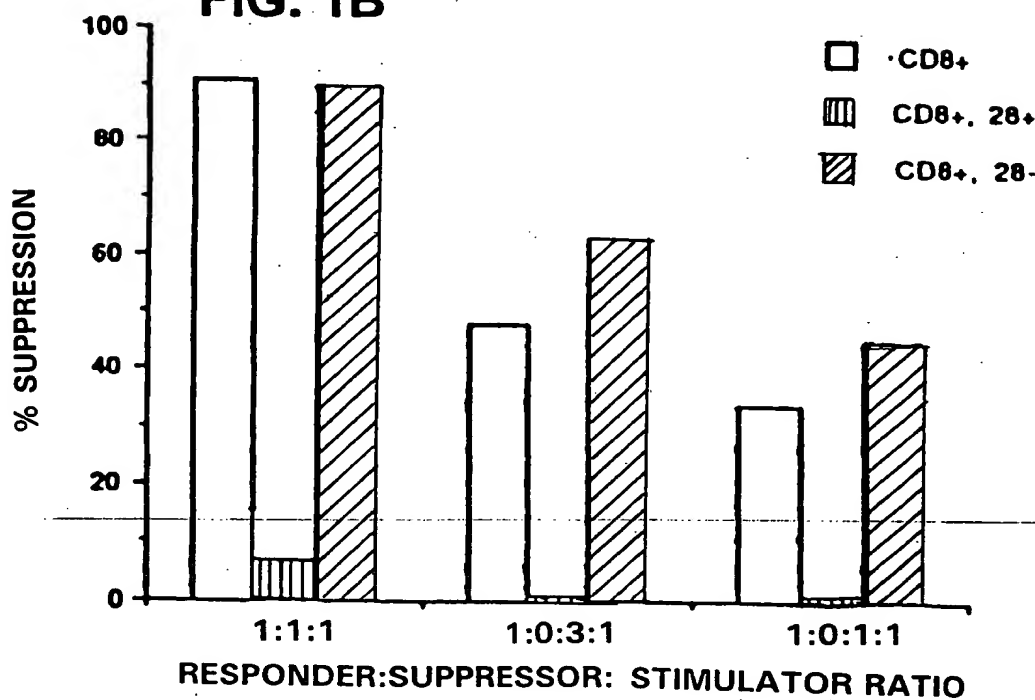


FIG. 1B



007227 " TFE94260

FIG. 1C

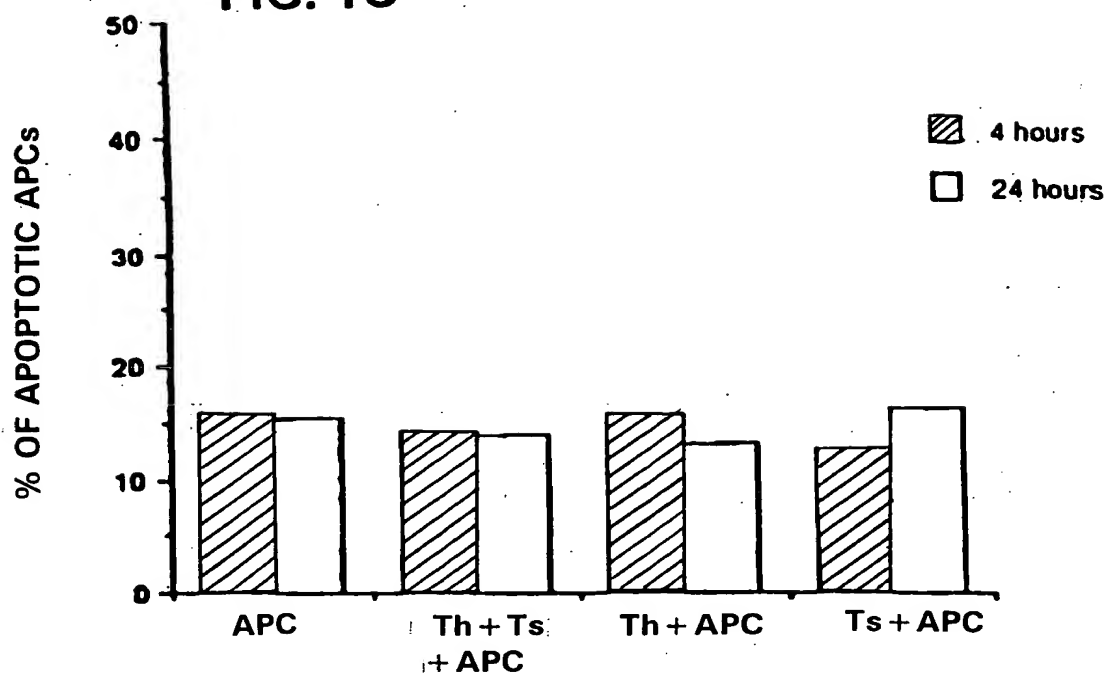


FIG. 1D

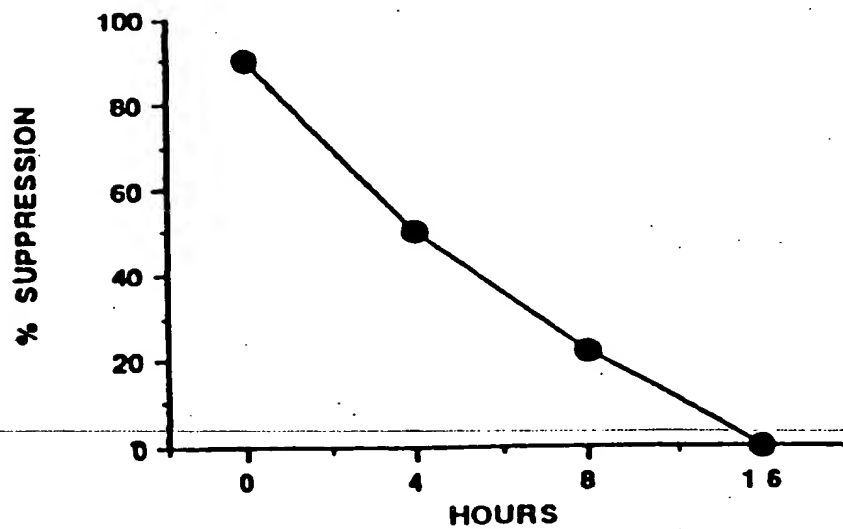


FIG. 2A

A

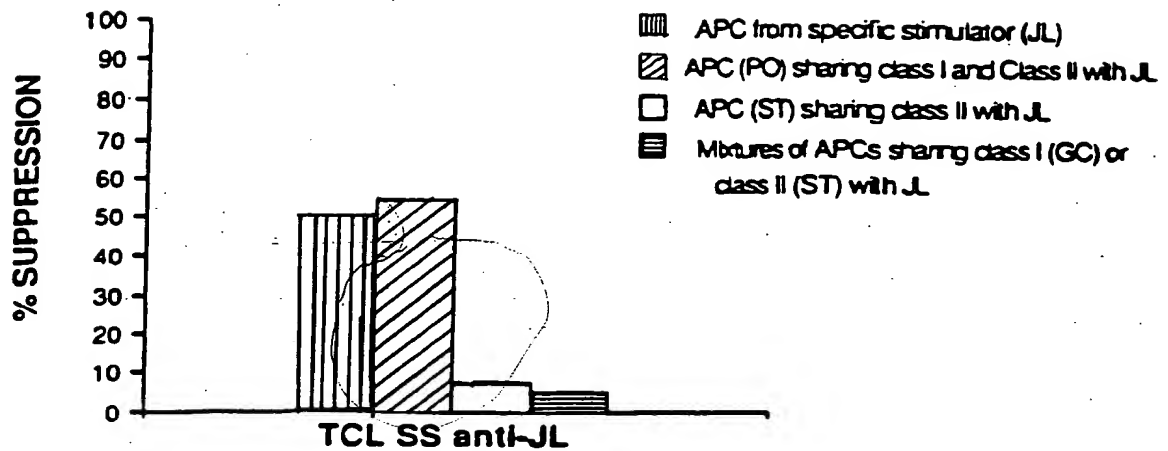


FIG. 2B

B

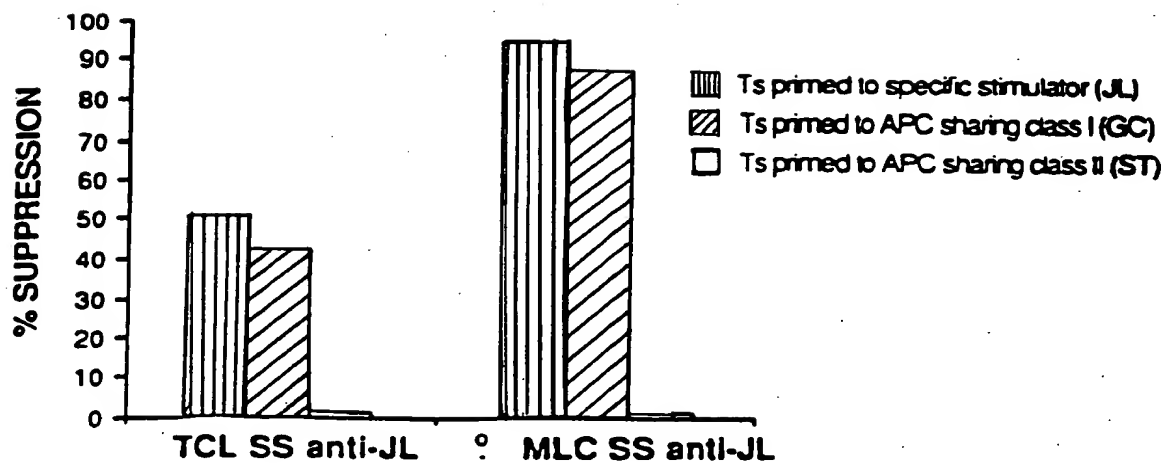
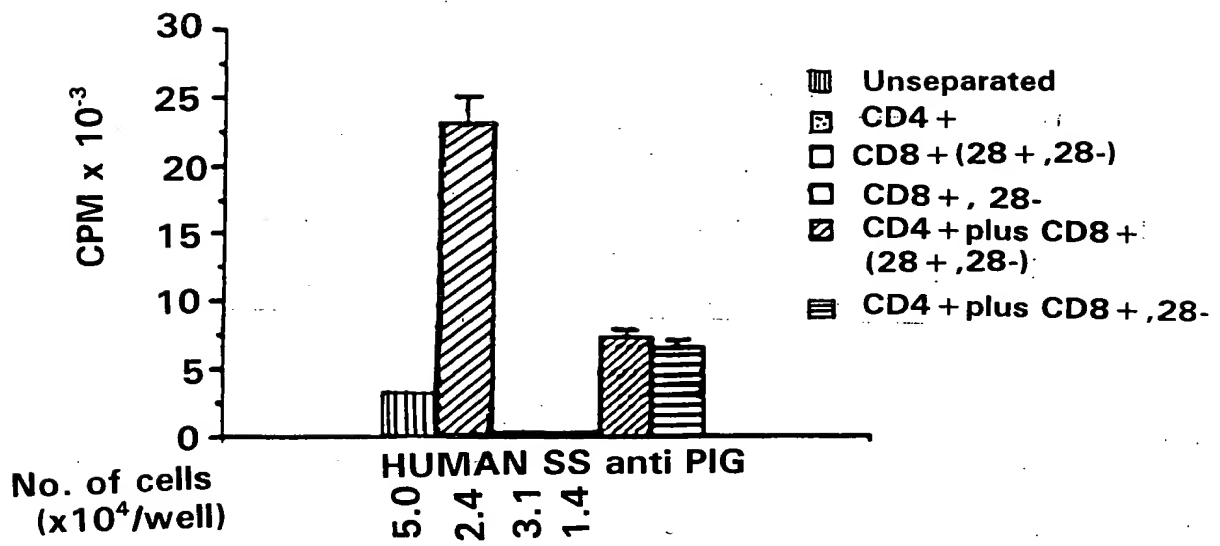


FIG. 3



5/73

FIG. 4A

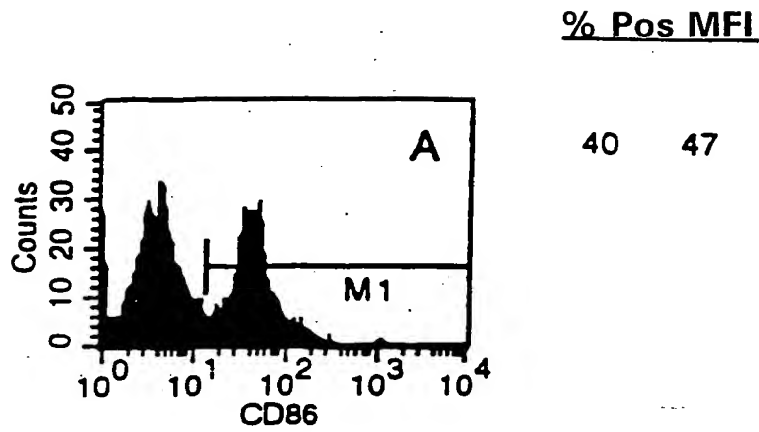


FIG. 4B

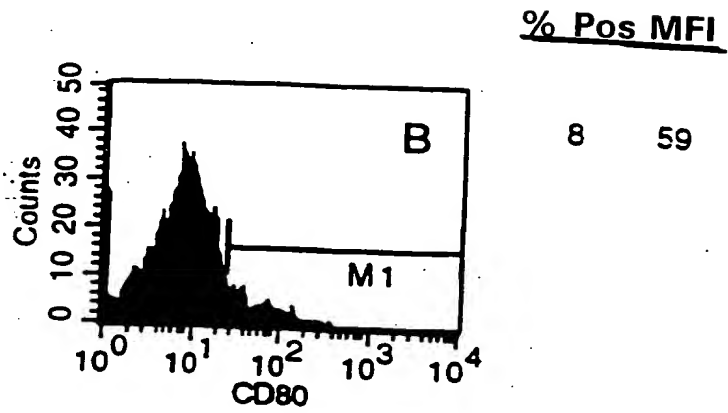


FIG. 4C

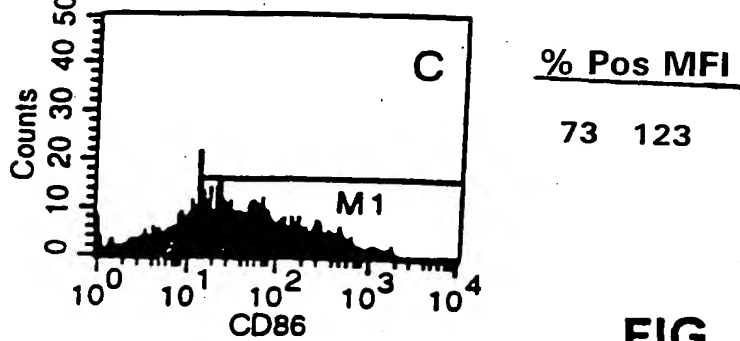
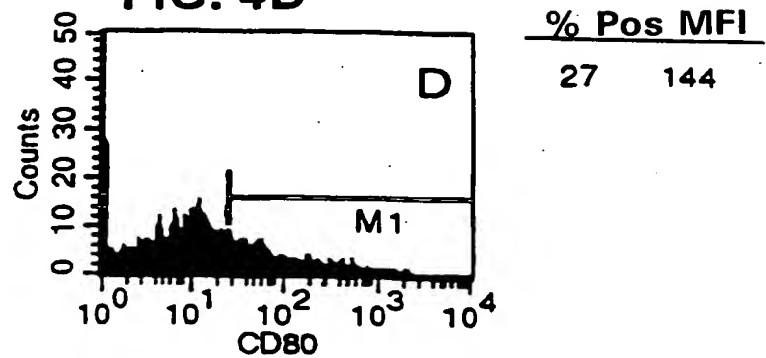


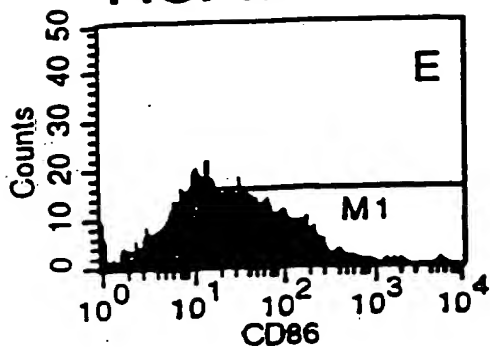
FIG. 4D



001221" TFE94260

6/73

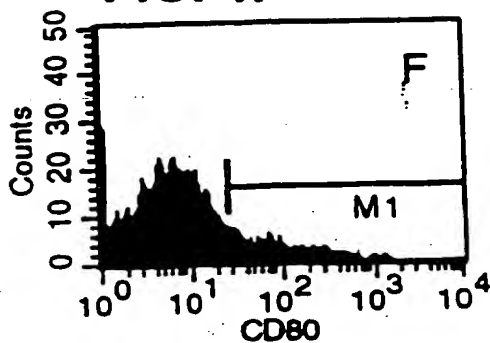
FIG. 4E



% Pos MFI

63 78

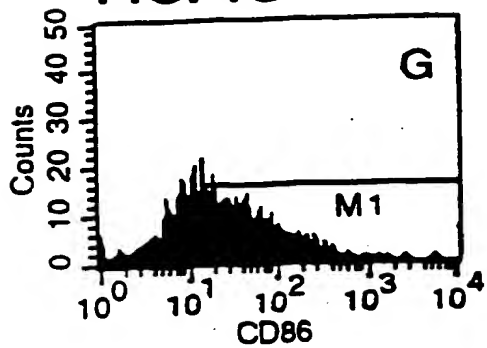
FIG. 4F



% Pos MFI

13 128

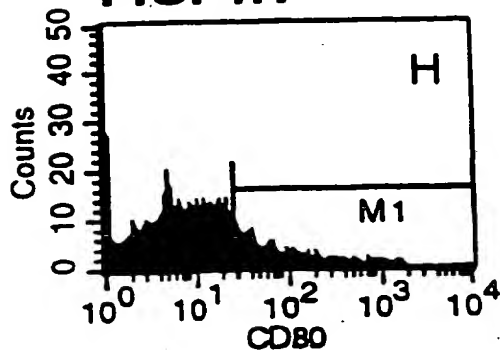
FIG. 4G



% Pos MFI

61 74

FIG. 4H



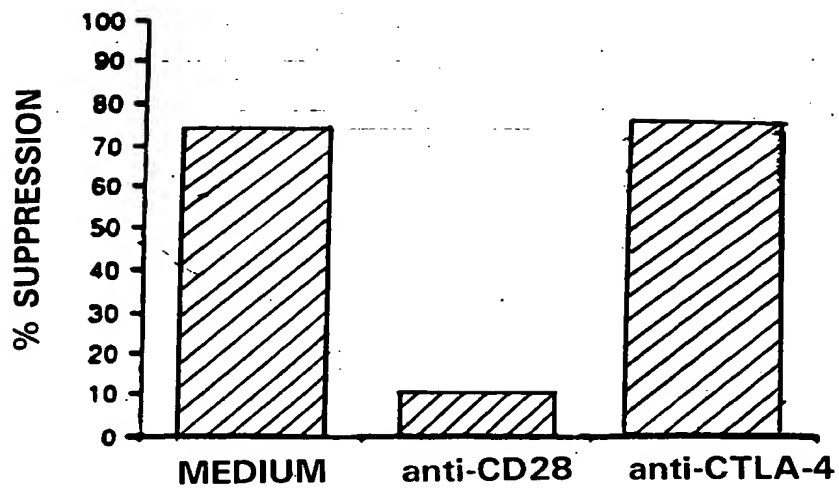
% Pos MFI

17 110

001221" TFE94260

7/73

FIG. 5



8/73

FIG. 6A

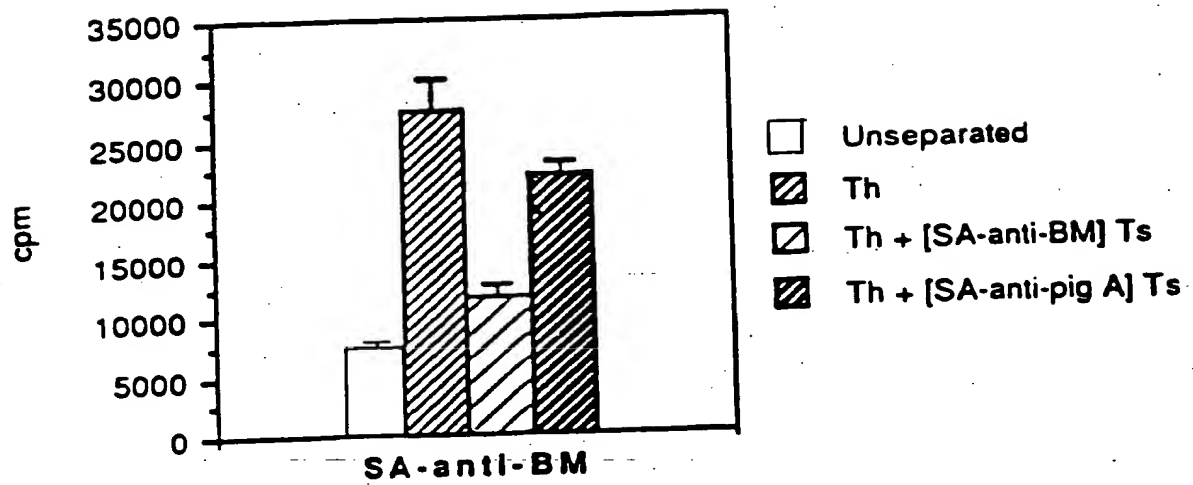
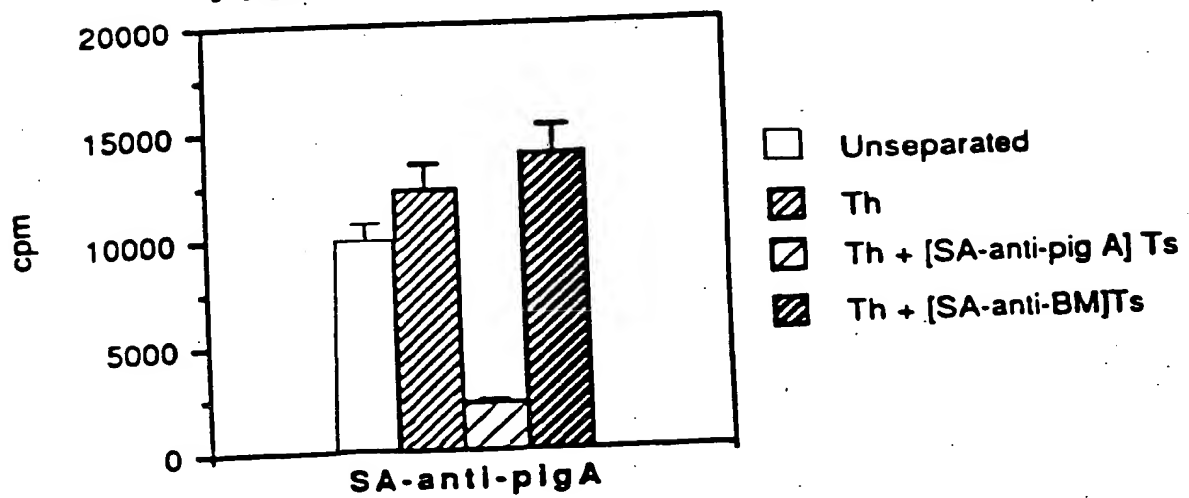


FIG. 6B



9/73

FIG. 7A

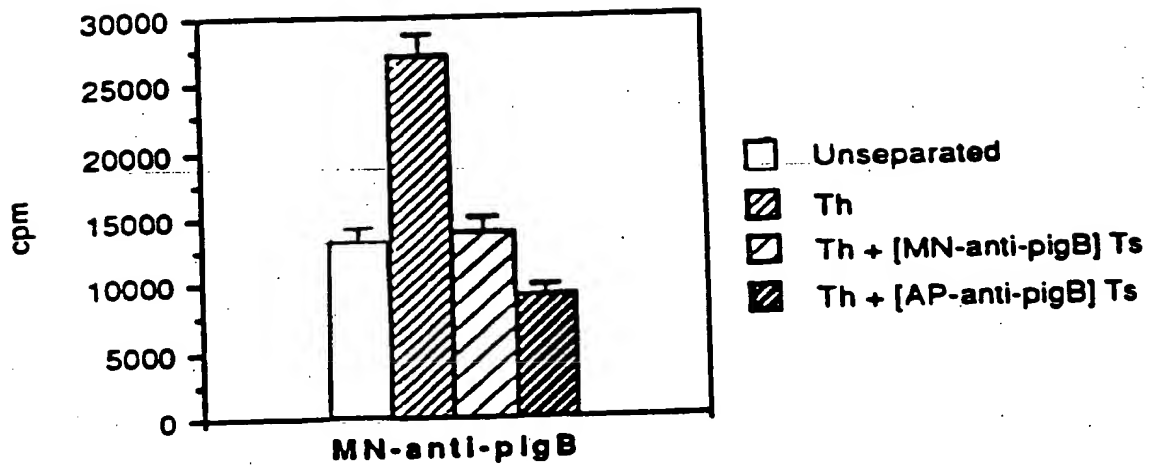
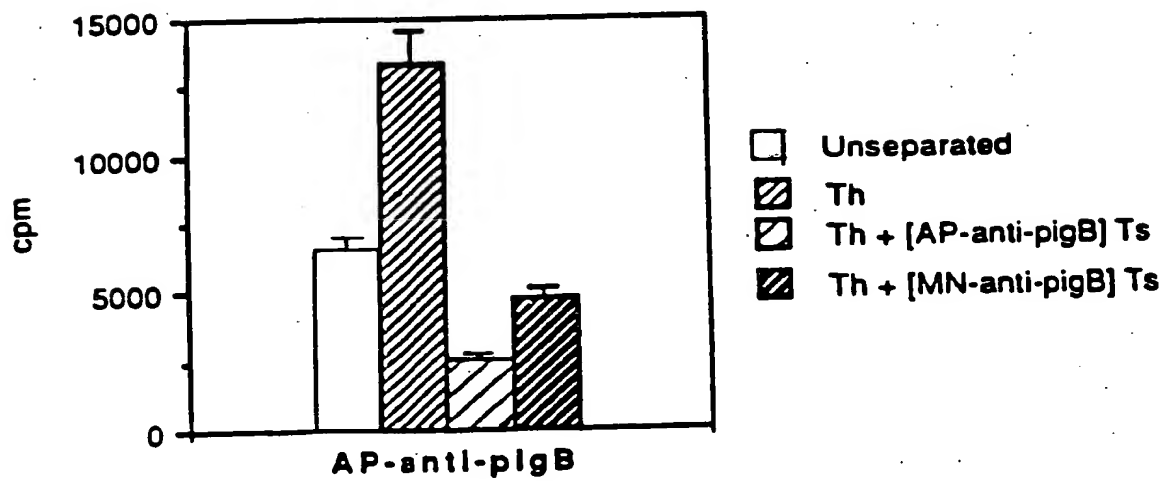


FIG. 7B



10/73

FIG. 8A

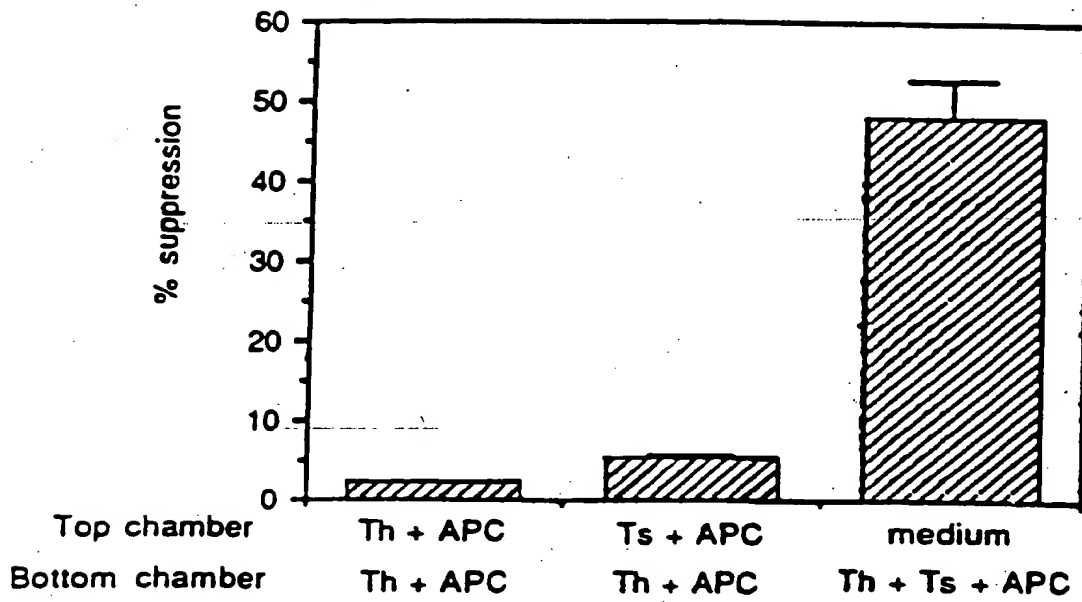
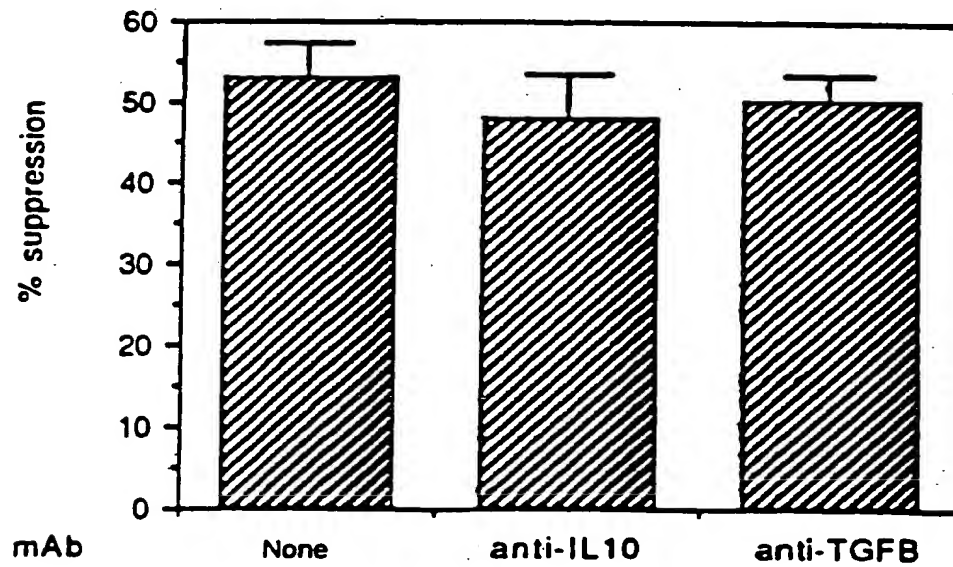


FIG. 8B



11/73

T helper cells

FIG. 9A

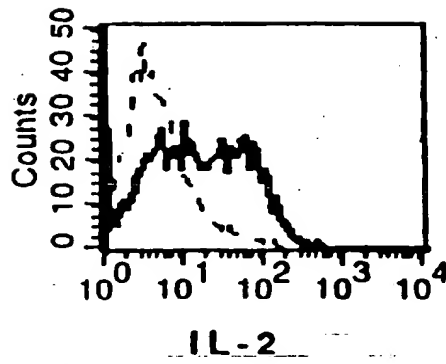


FIG. 9B

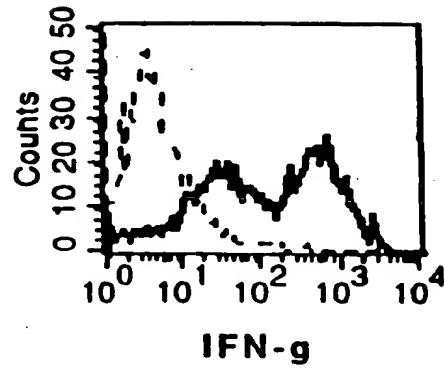


FIG. 9C

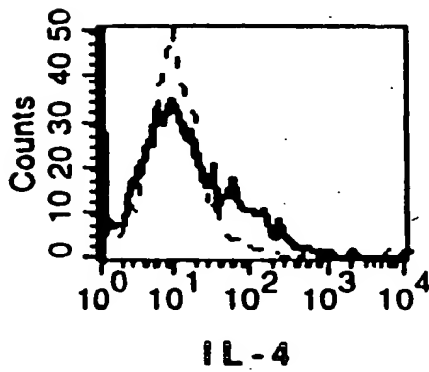
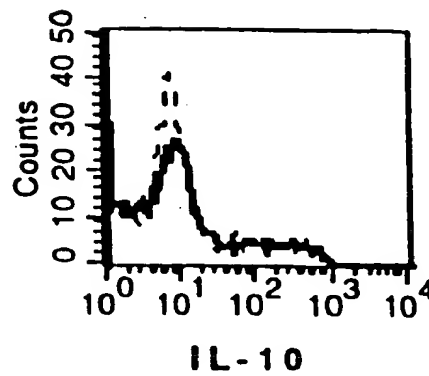
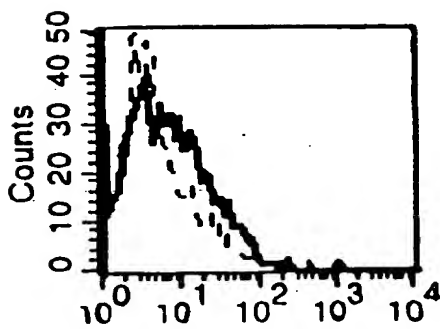


FIG. 9D



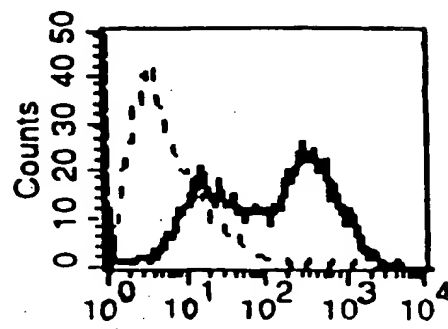
12/73

T suppressor cells



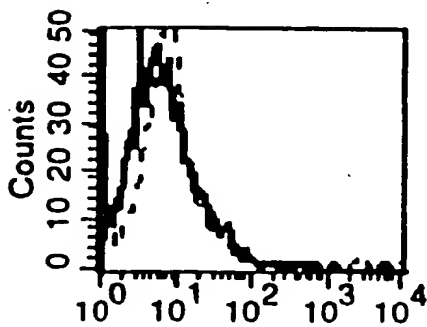
IL-2

FIG. 9E



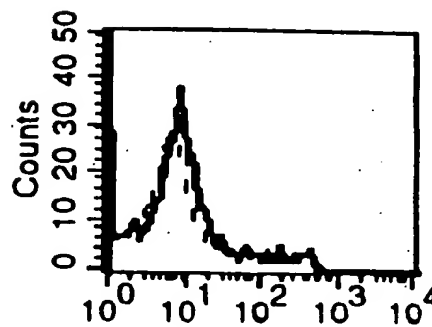
IFN-g

FIG. 9F



IL-4

FIG. 9G



IL-10

FIG. 9H

007227 " TFE94260

13/73

FIG. 10A

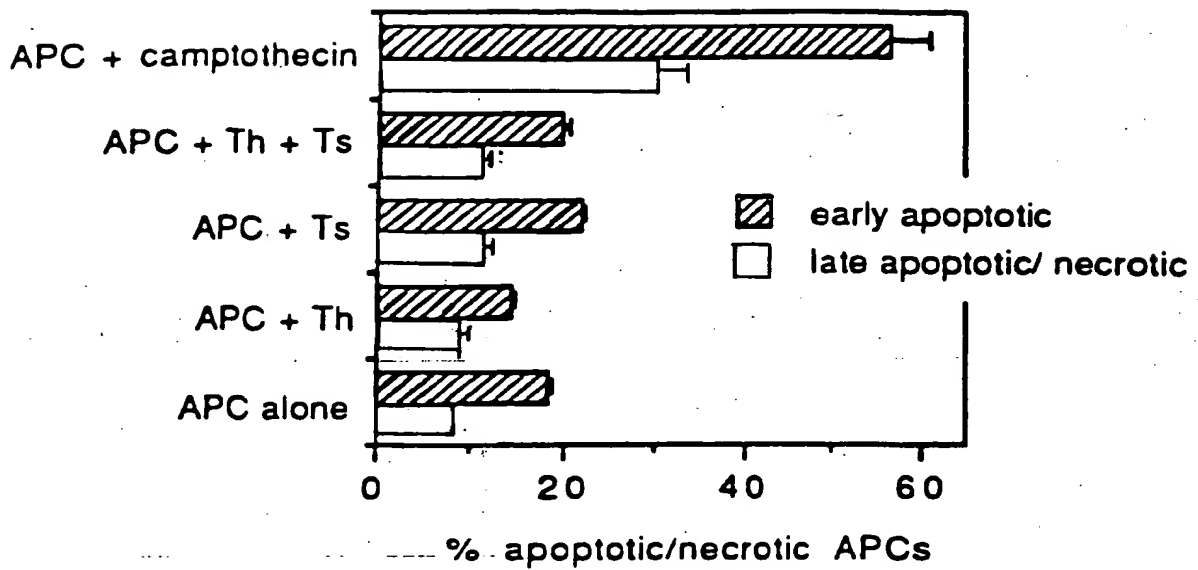


FIG. 10B

Effector/
Target

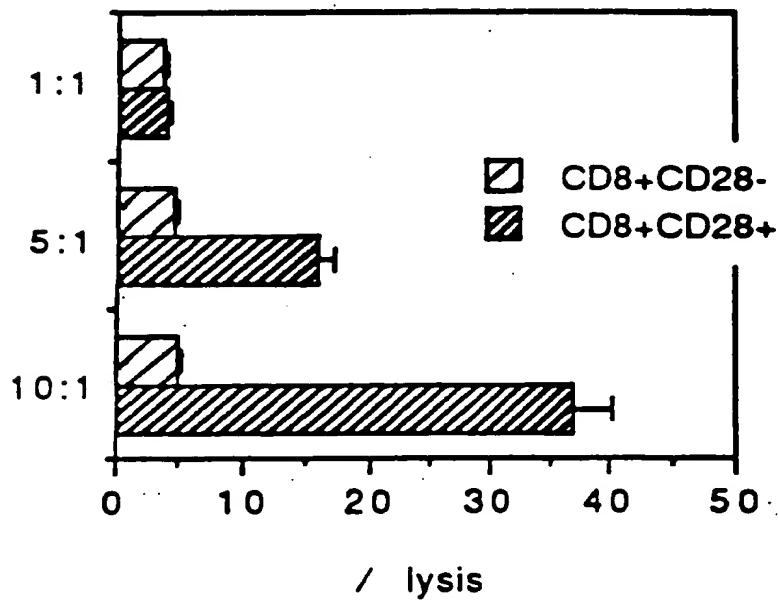
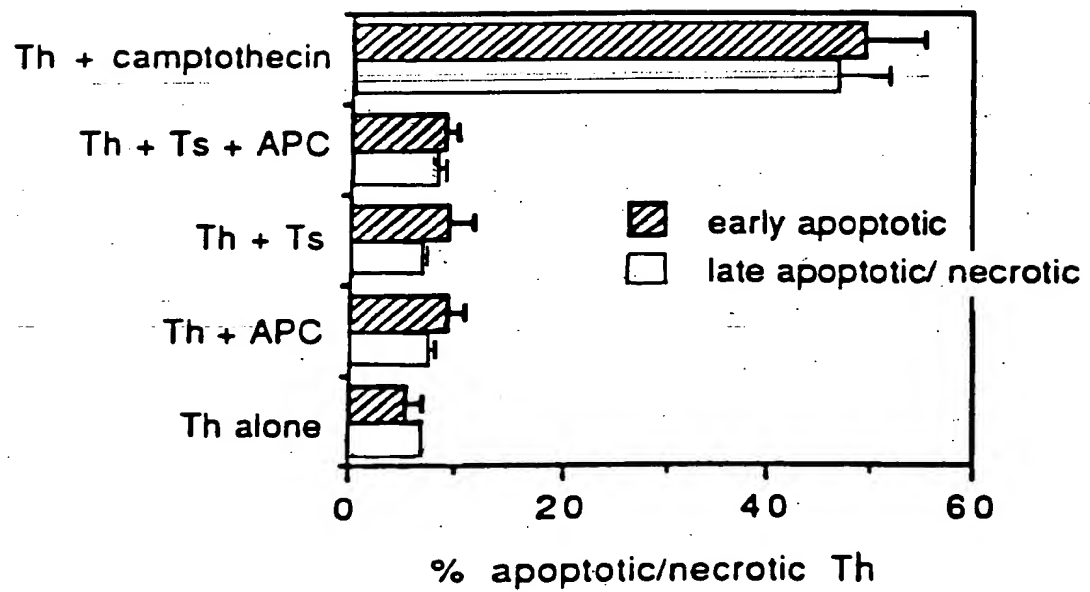


FIG. 10C



15/73

FIG. 11A

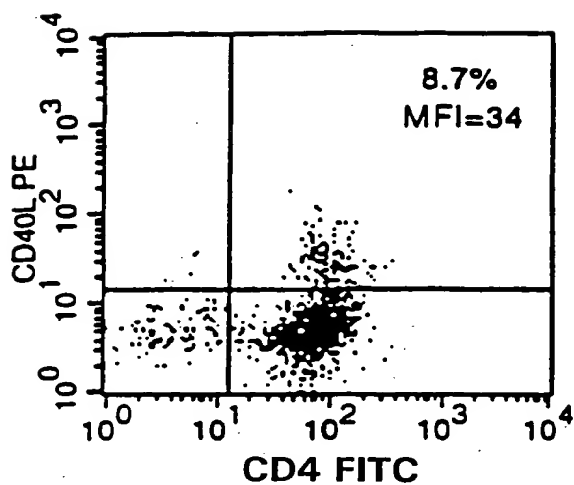


FIG. 11B

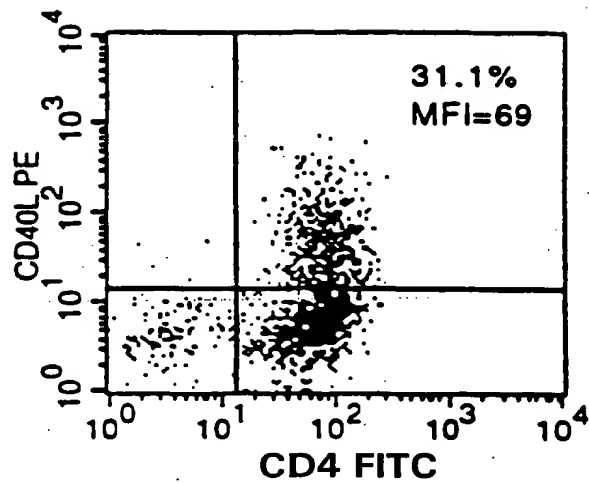


FIG. 11C

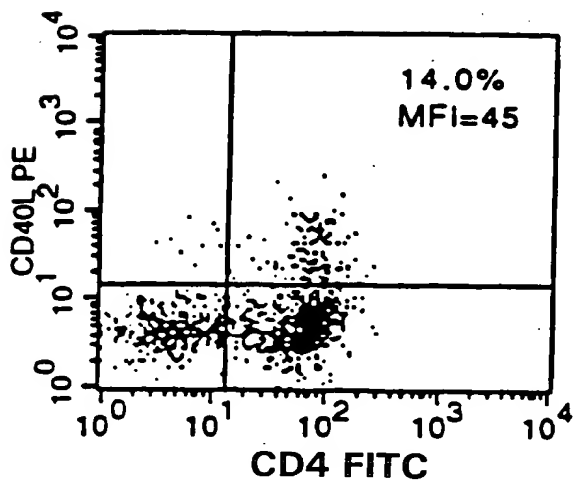
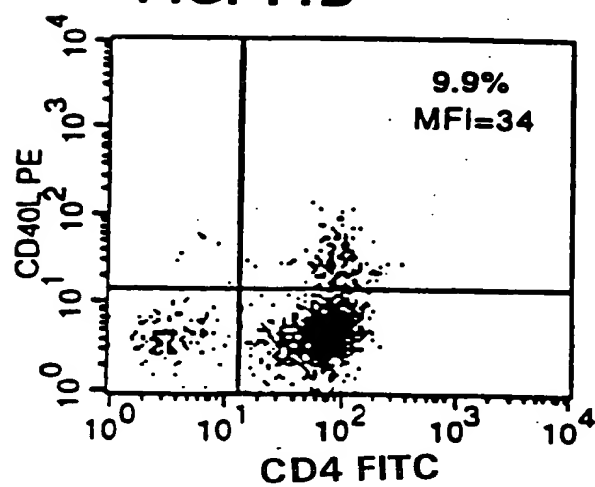
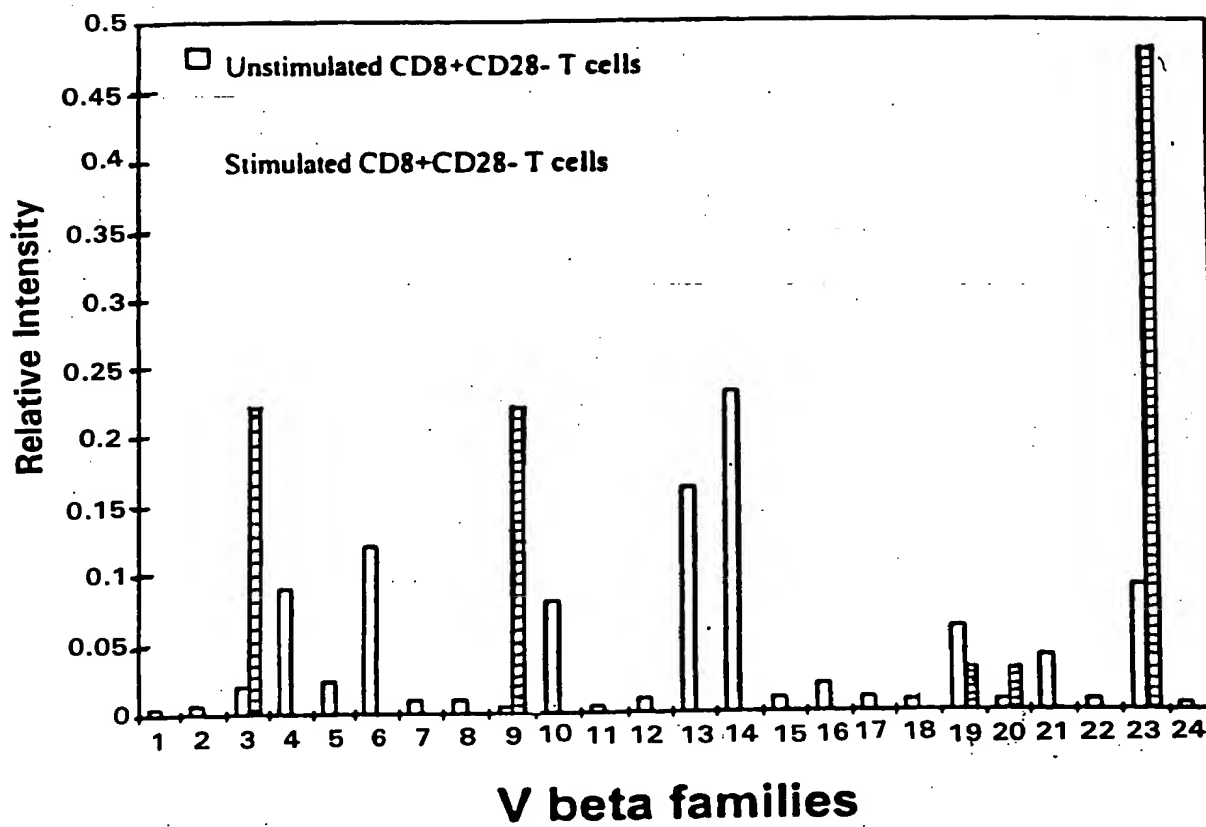


FIG. 11D



16/73

FIG. 12



17/73

FIG. 13A

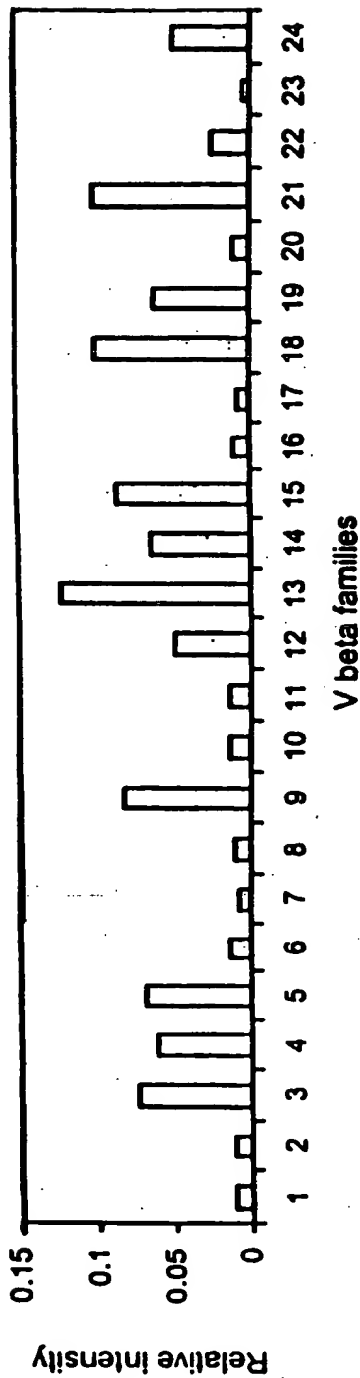
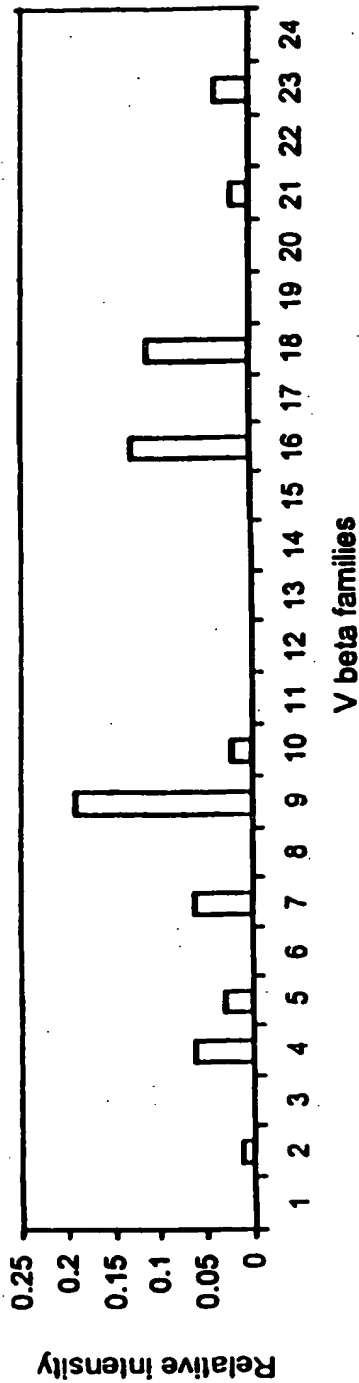


FIG. 13B



18/73

FIG. 13C

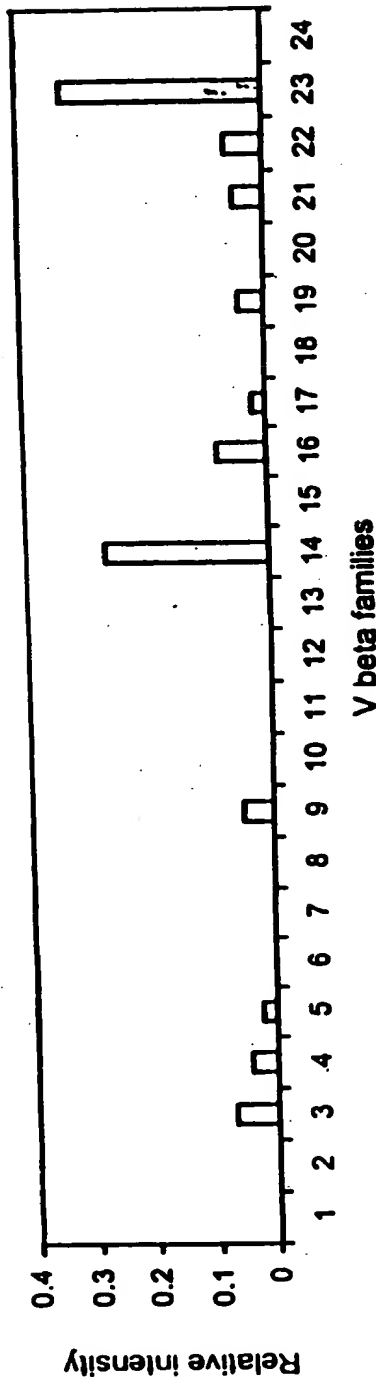
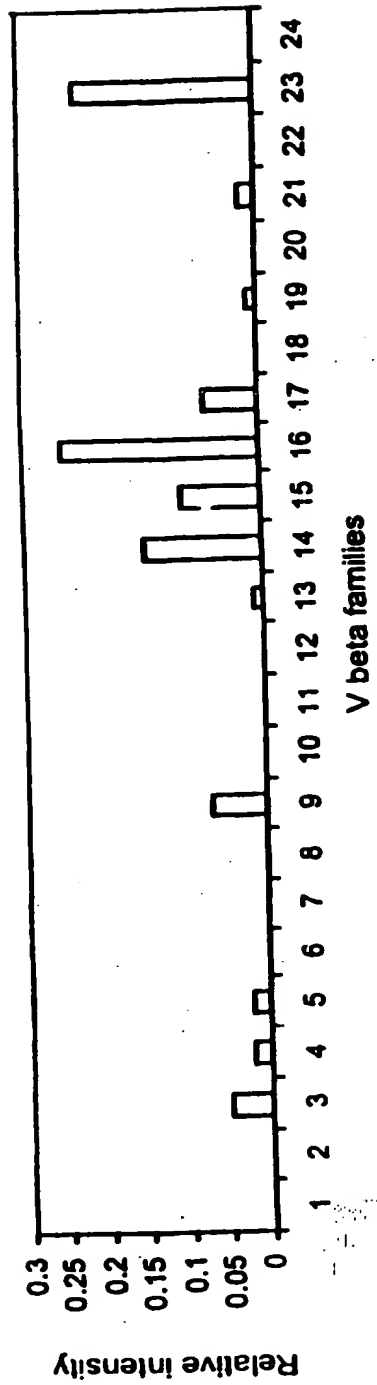


FIG. 13D



19/73

FIG. 14A

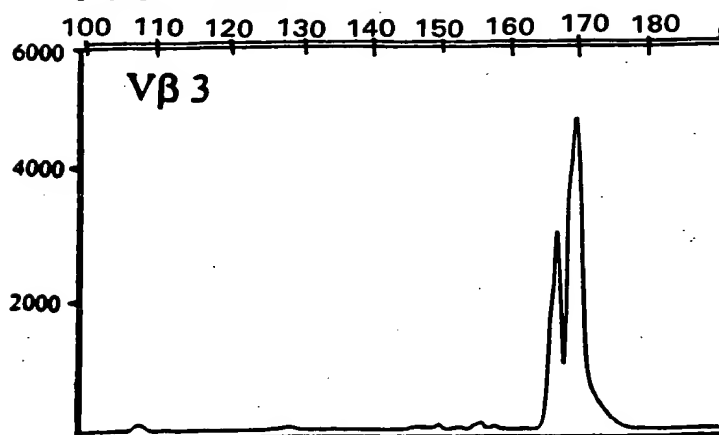


FIG. 14B

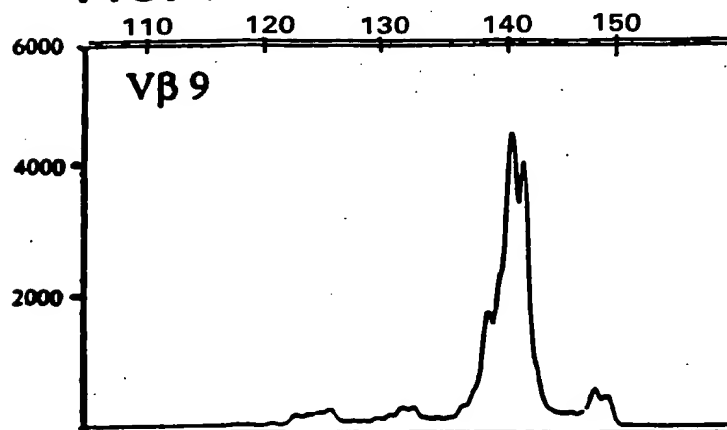
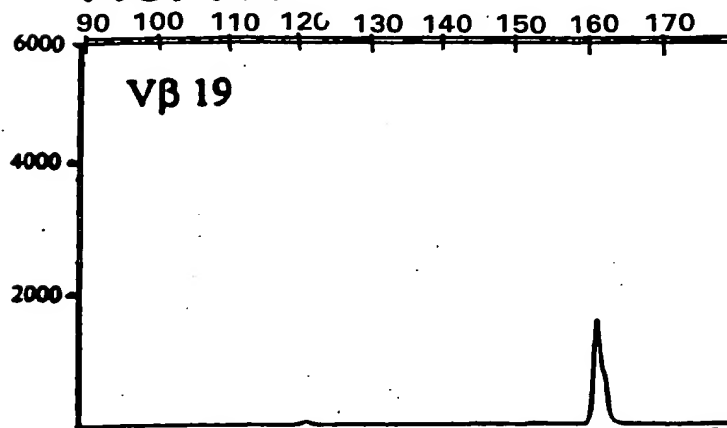


FIG. 14C



0074631-12100

20/73

FIG. 14D

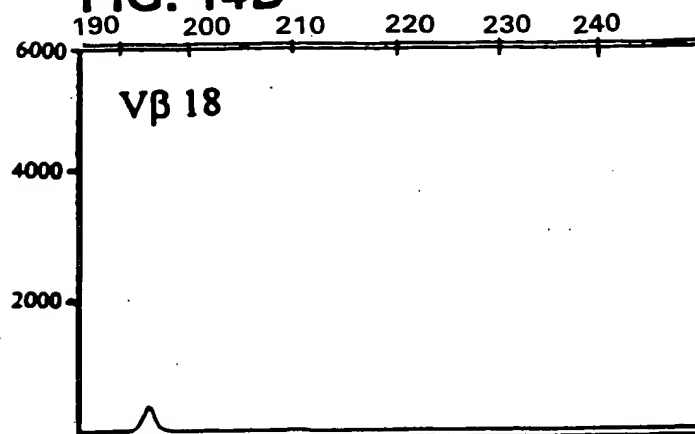


FIG. 14E

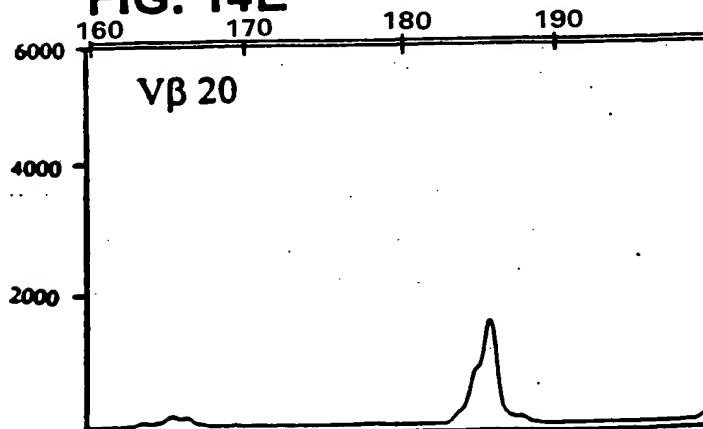
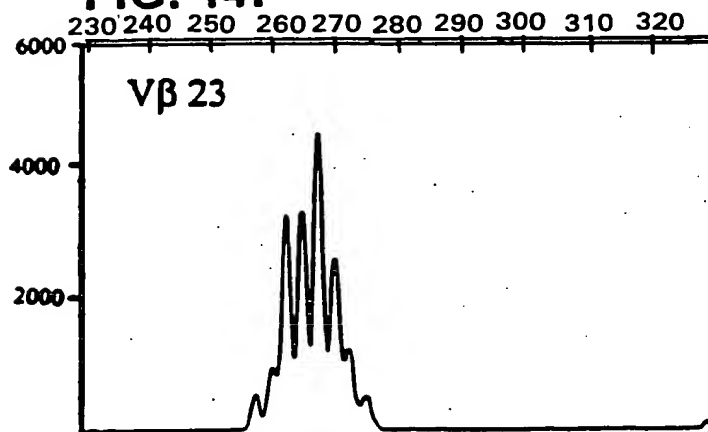


FIG. 14F



004631.122100

21/73

FIG. 15A

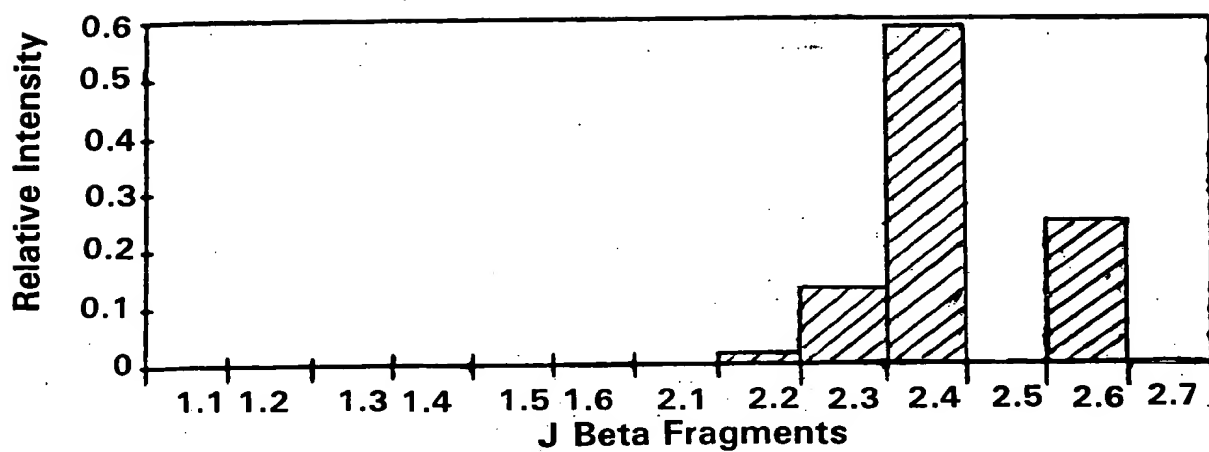


FIG. 15B

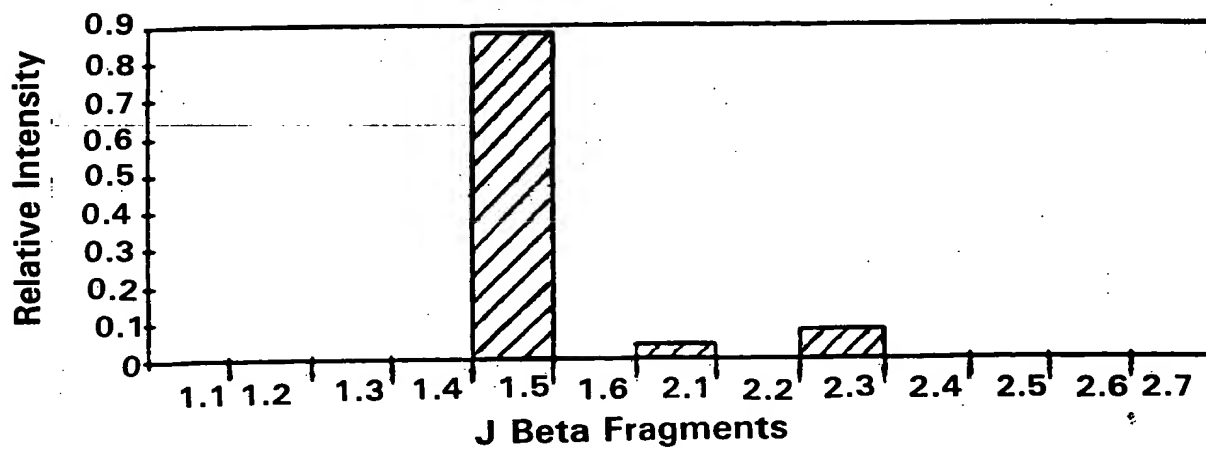
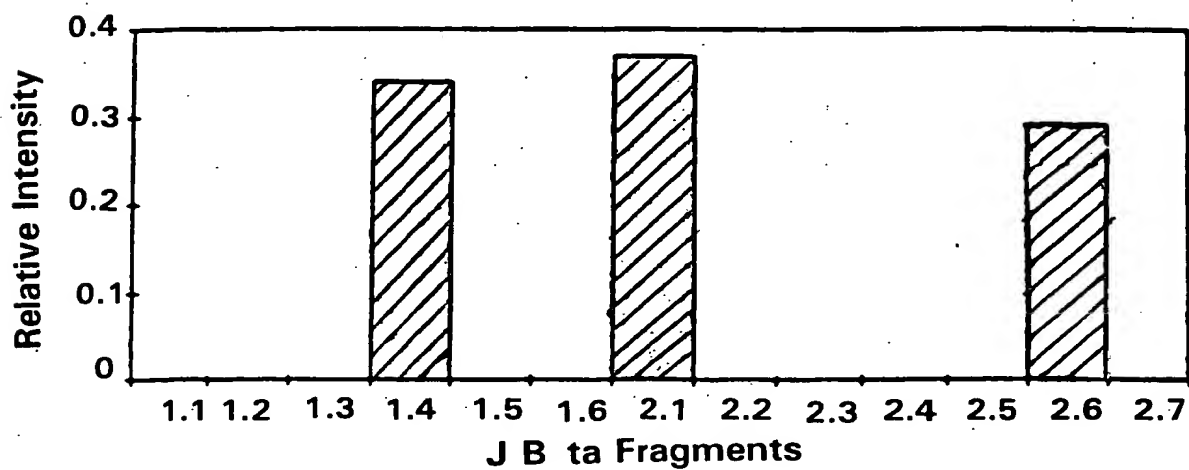
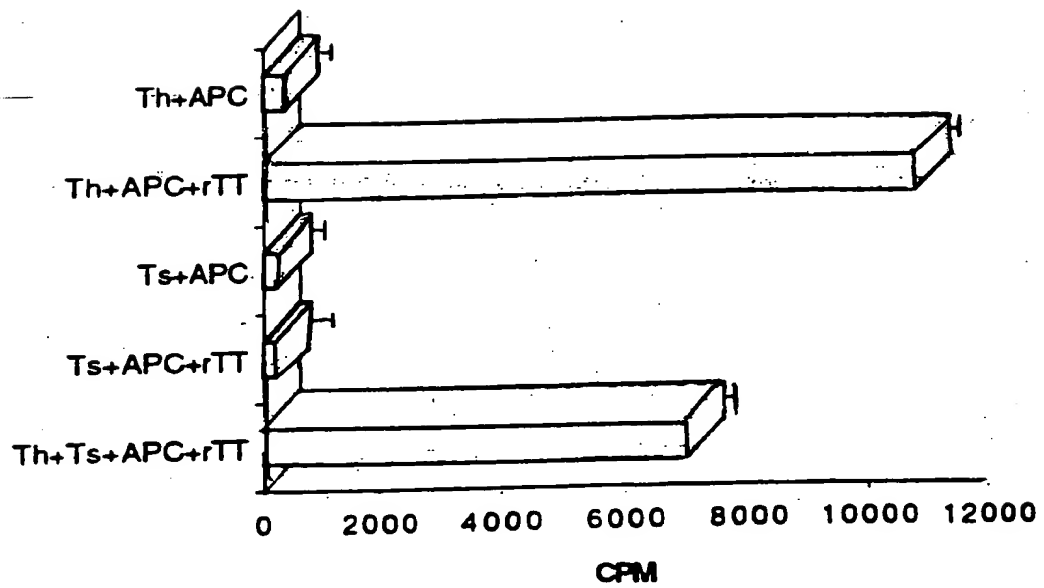


FIG. 15C



22/73

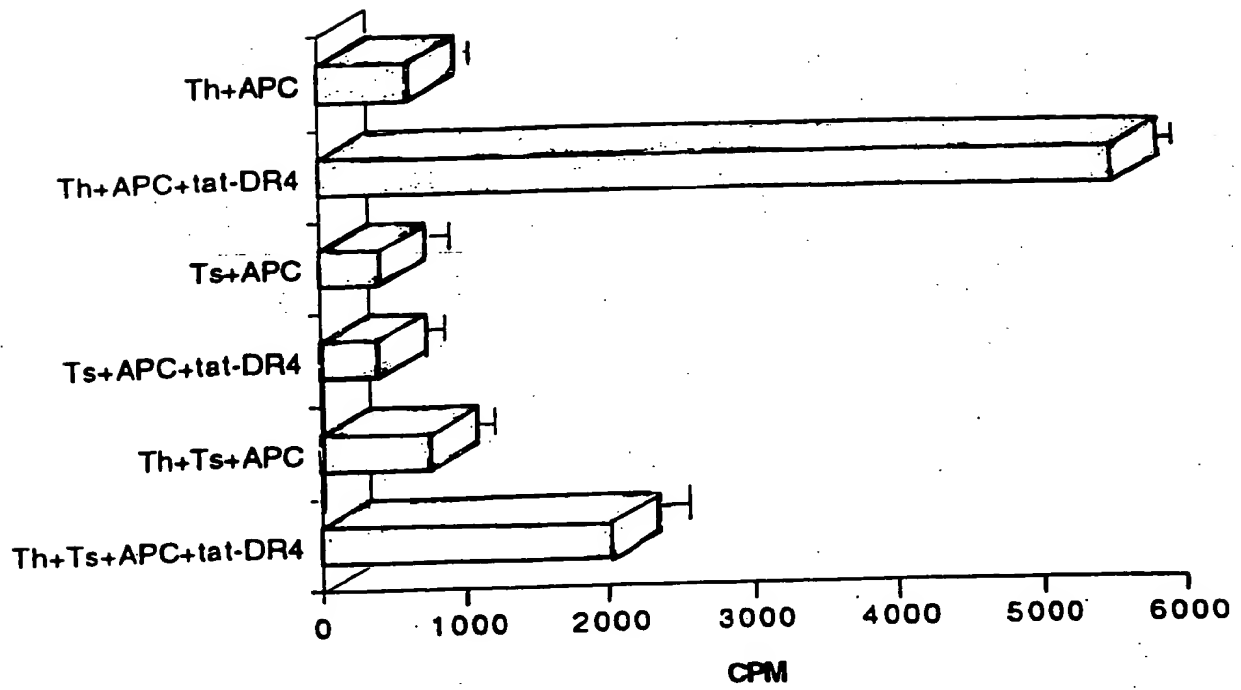
FIG. 16



0946311-122100

23/73

FIG. 17



09746344-123100

24/73

FIG. 18A

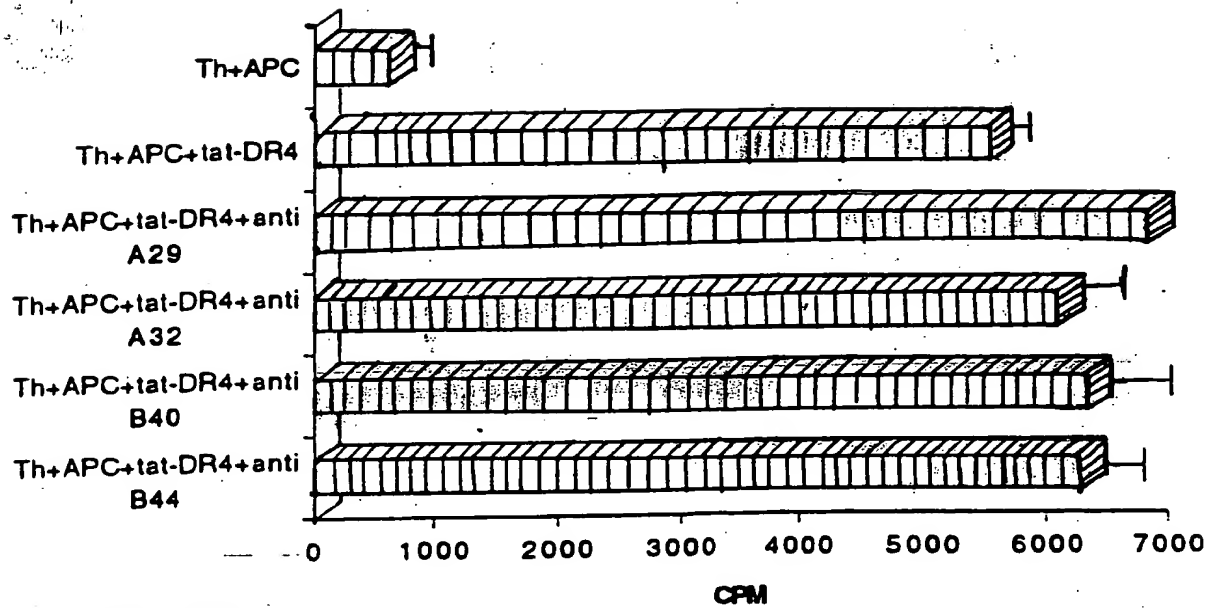
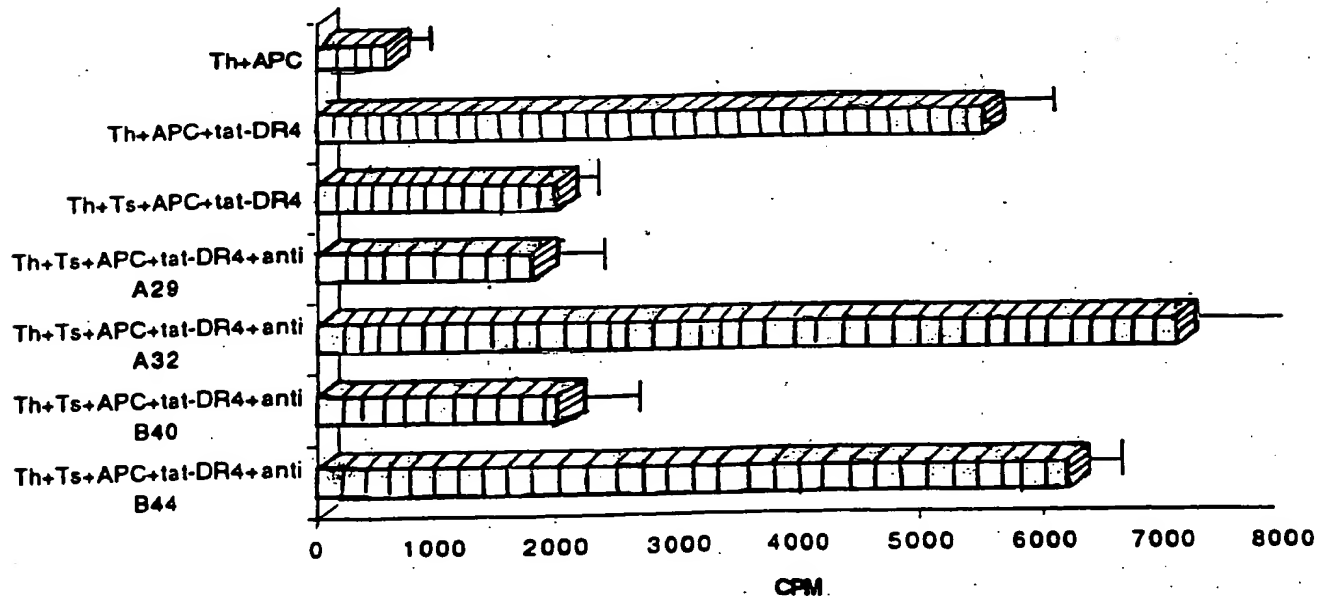


FIG. 18B



25/73

FIG. 19A-1

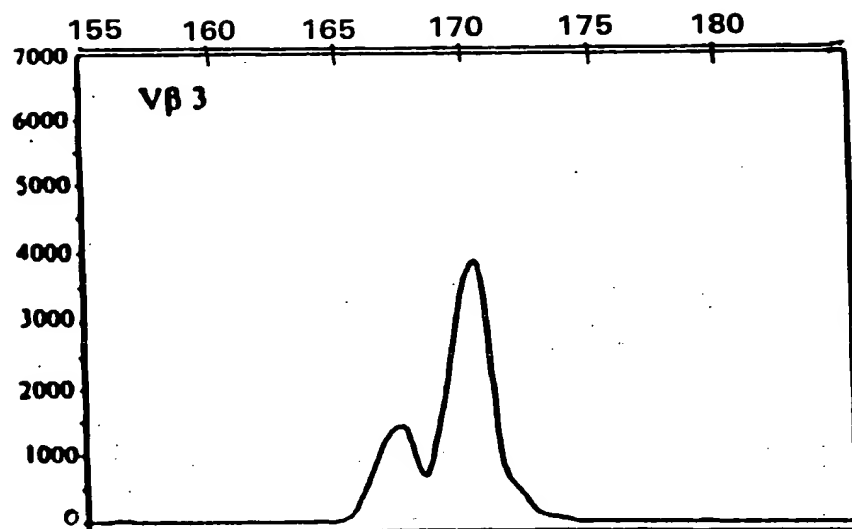


FIG. 19A-2

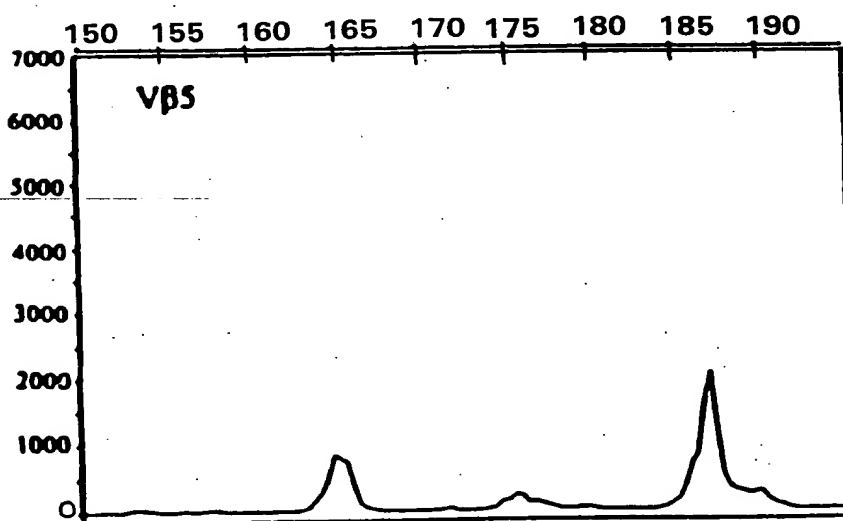
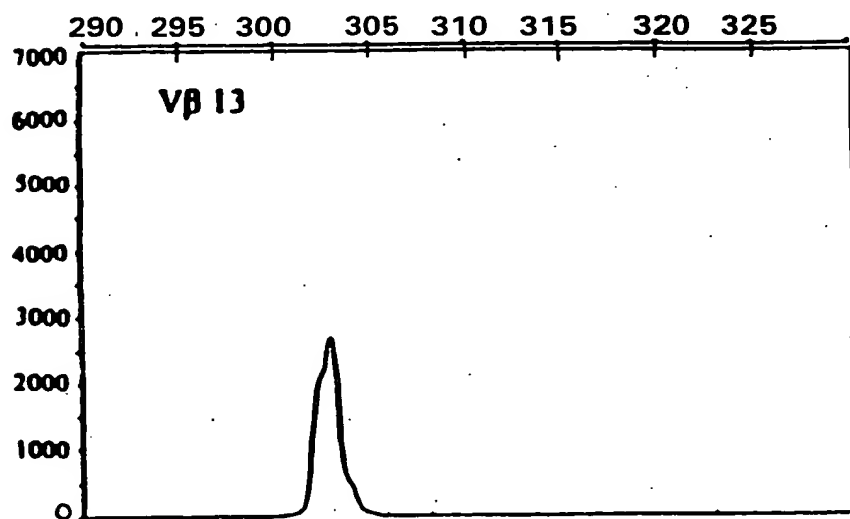


FIG. 19A-3



26/73

FIG. 19A-4

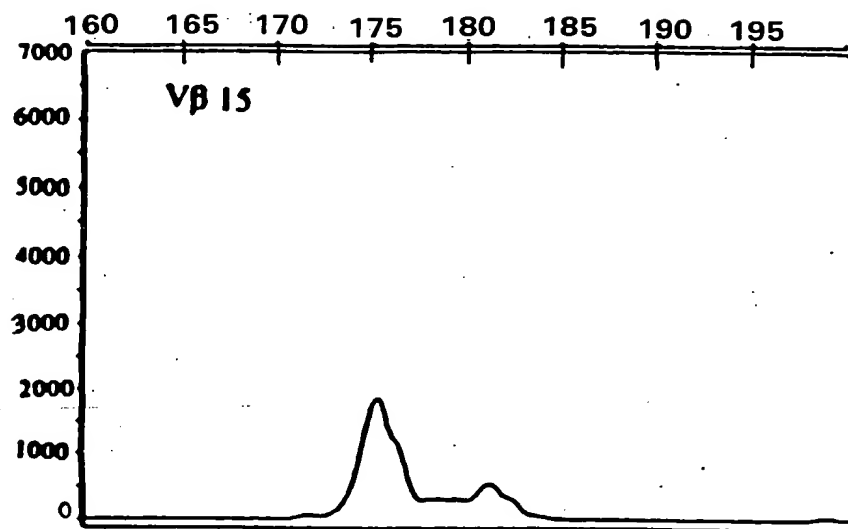
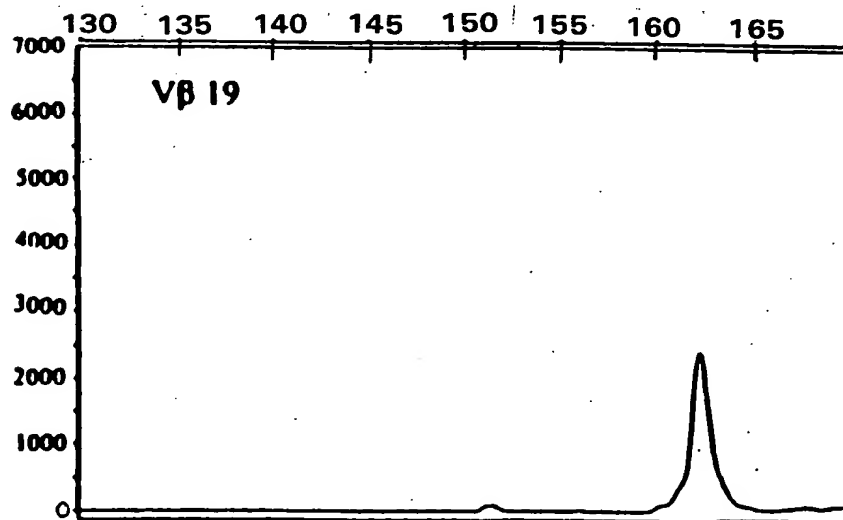


FIG. 19A-5



27/73

FIG. 19B-1

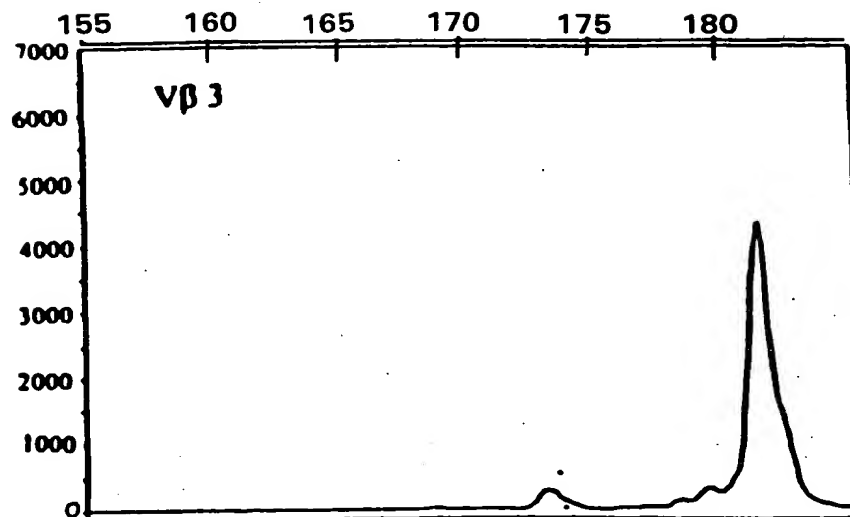


FIG. 19B-2

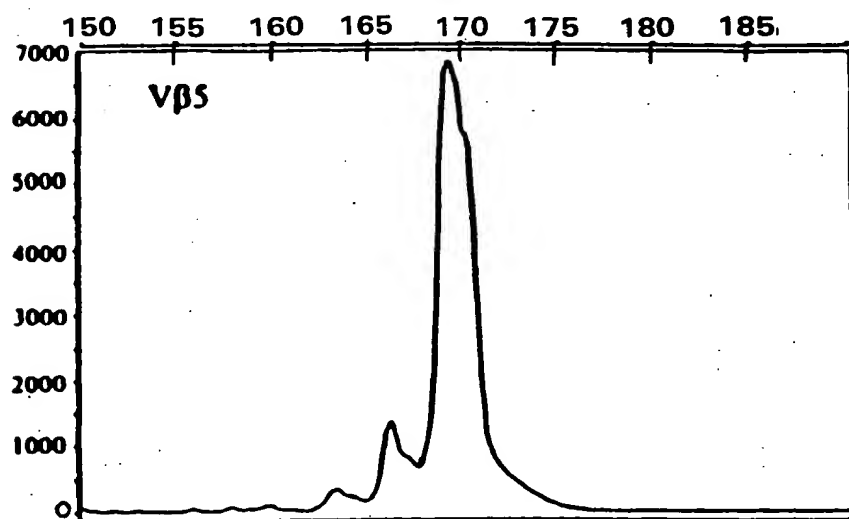
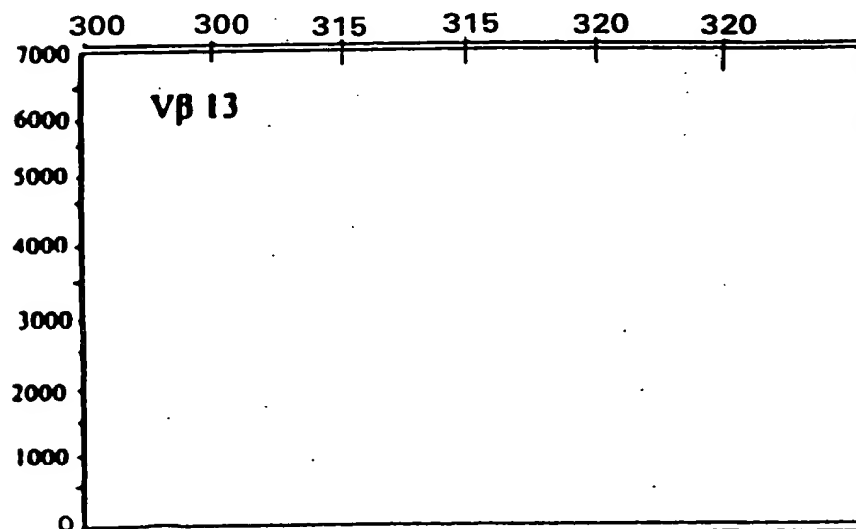


FIG. 19B-3



09746344-122100

28/73

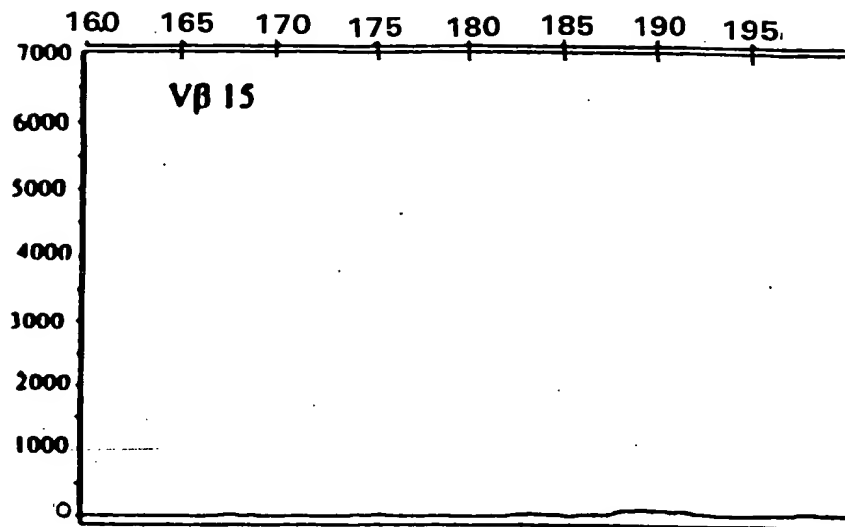


FIG. 19B-4

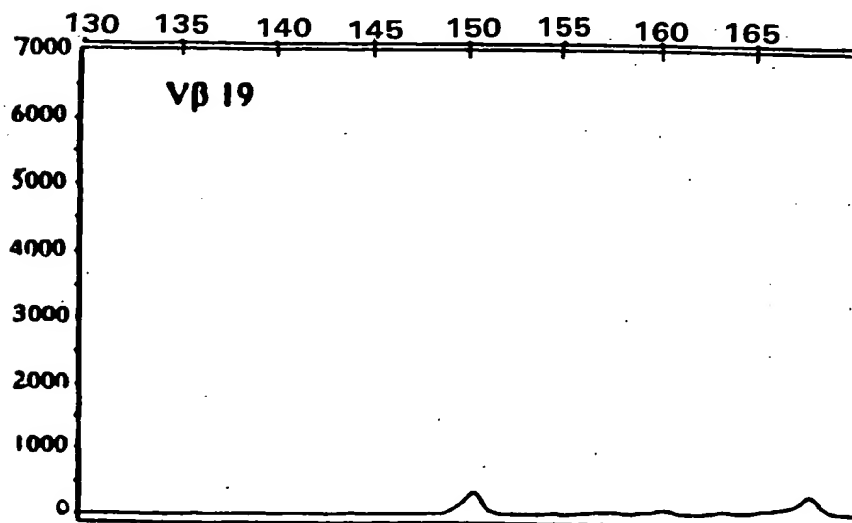


FIG. 19B-5

0946311-122100

30941-1200

FIG. 19C-1

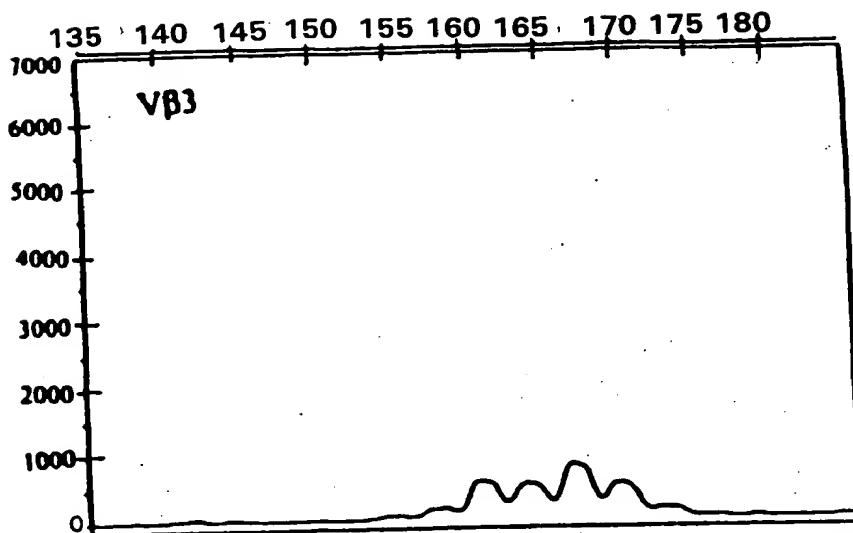


FIG. 19C-2

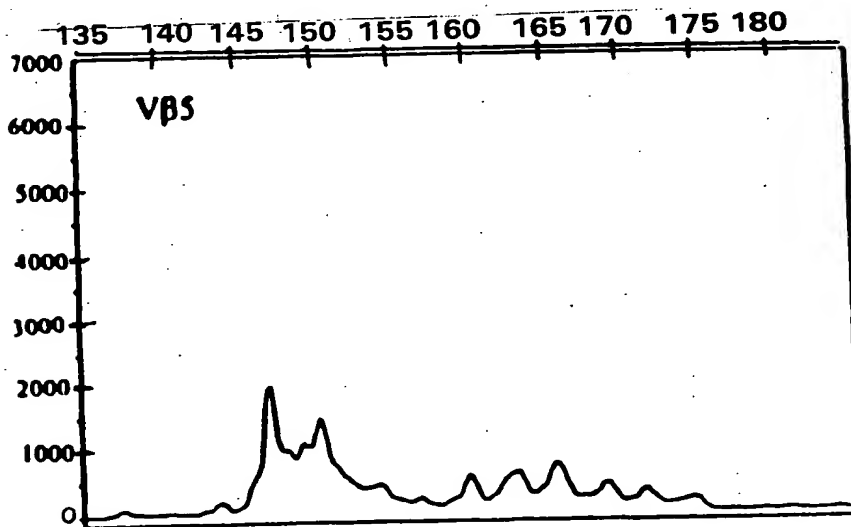
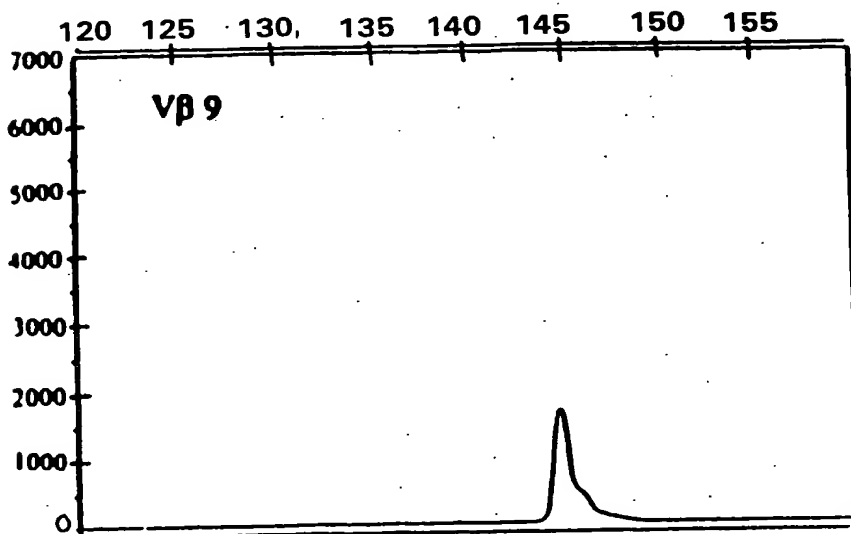


FIG.19C-3



30/73

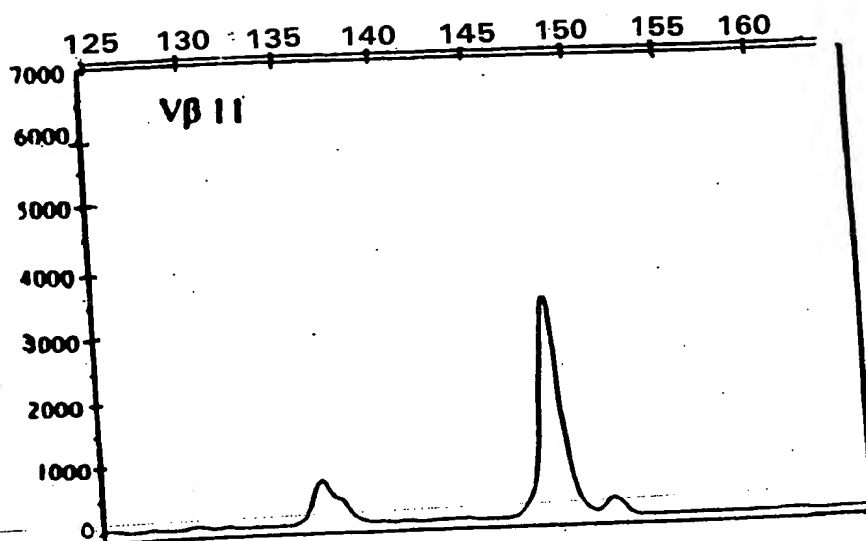


FIG. 19C-4

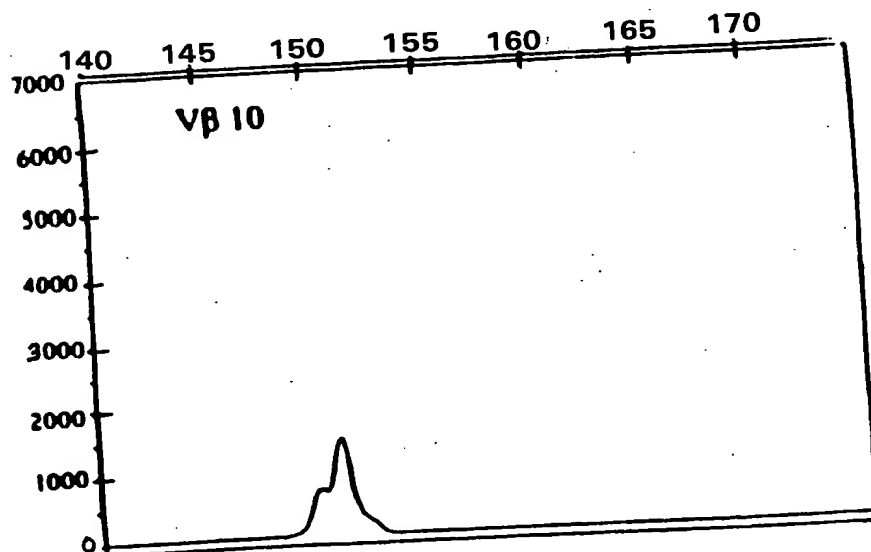


FIG. 19C-5

0946341-124100

31/73

FIG. 20A

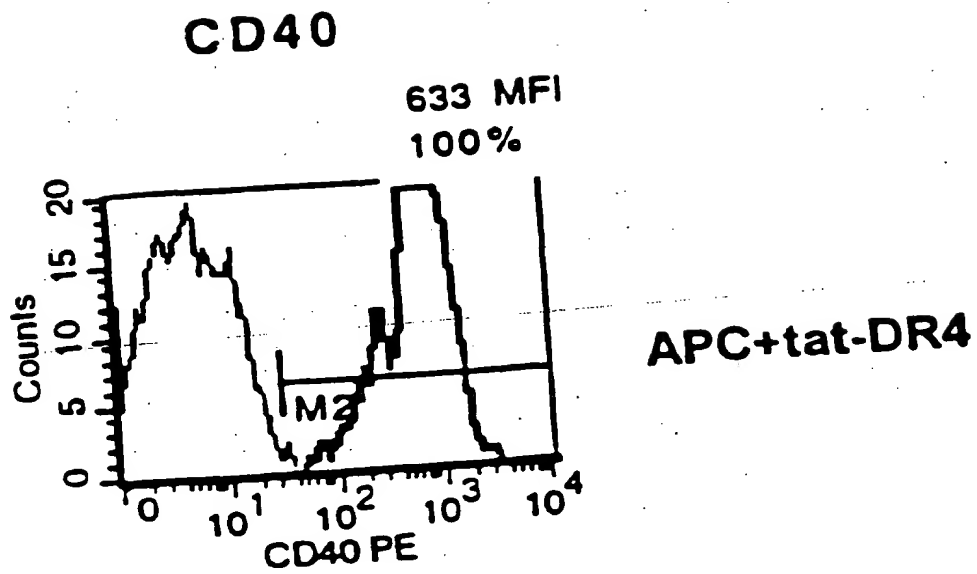
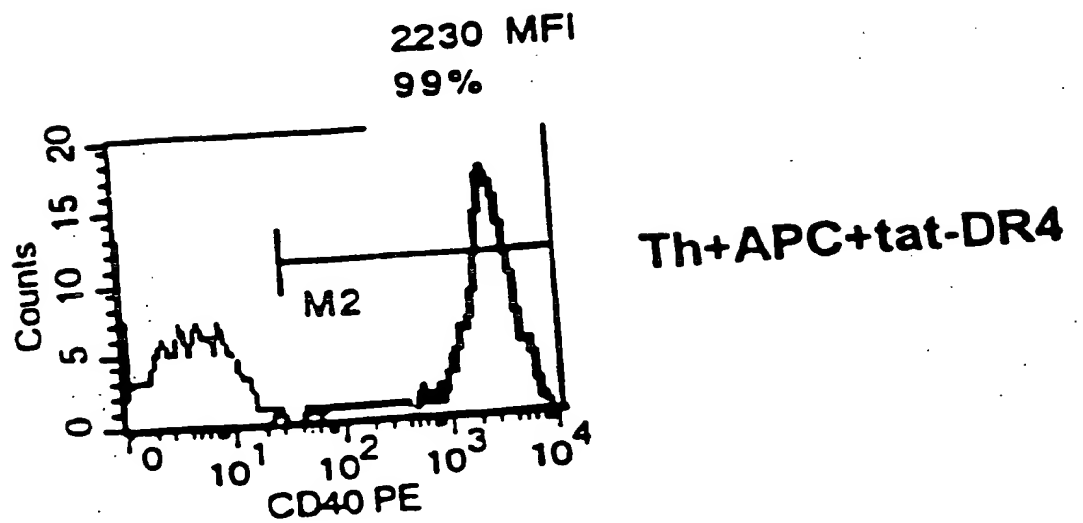


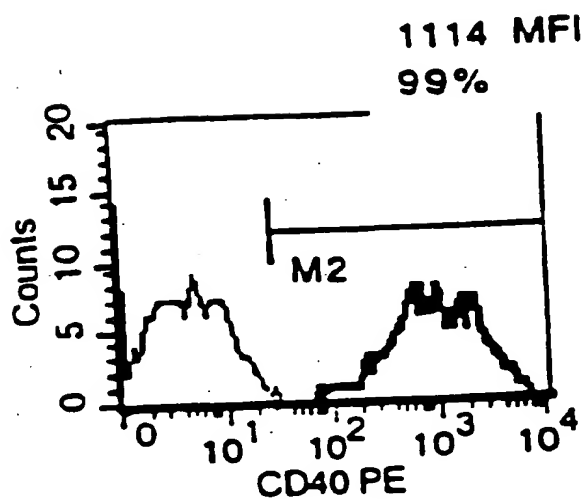
FIG. 20B



32/73

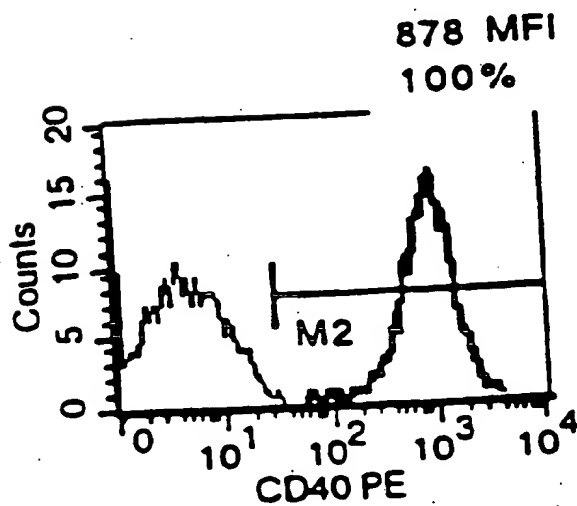
CD40

FIG. 20C



Th+Ts+APC+tat-DR4

FIG. 20D



Ts+APC+tat-DR4

007221" TTES4260

33/73

FIG. 20E

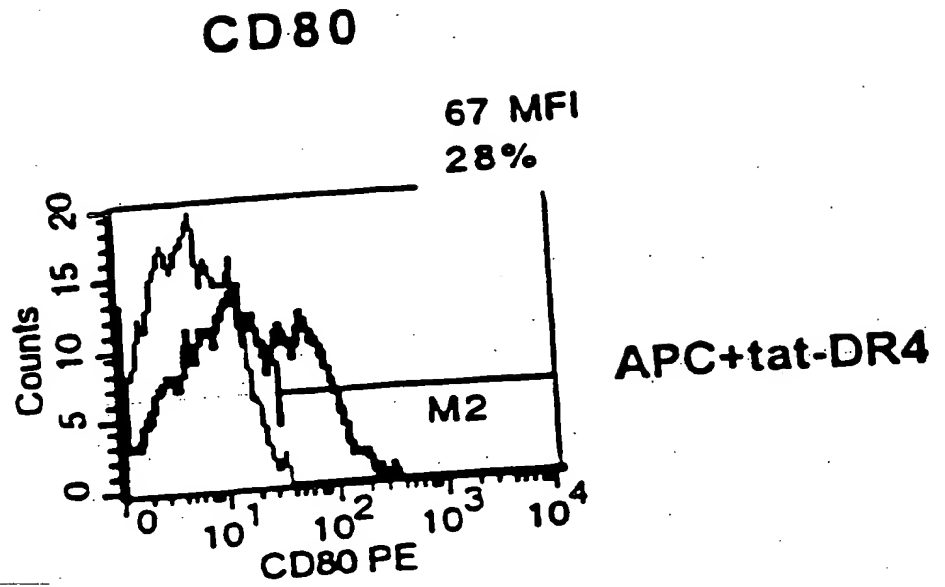
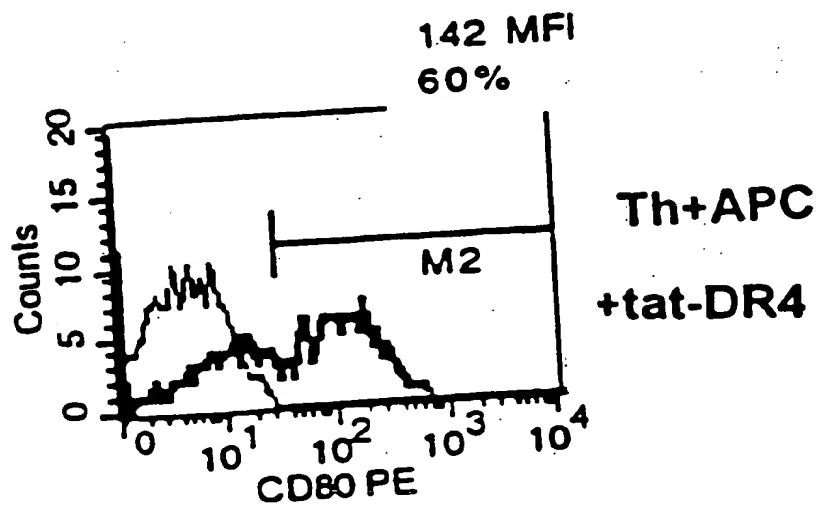


FIG. 20F



34/73

CD80

FIG. 20G

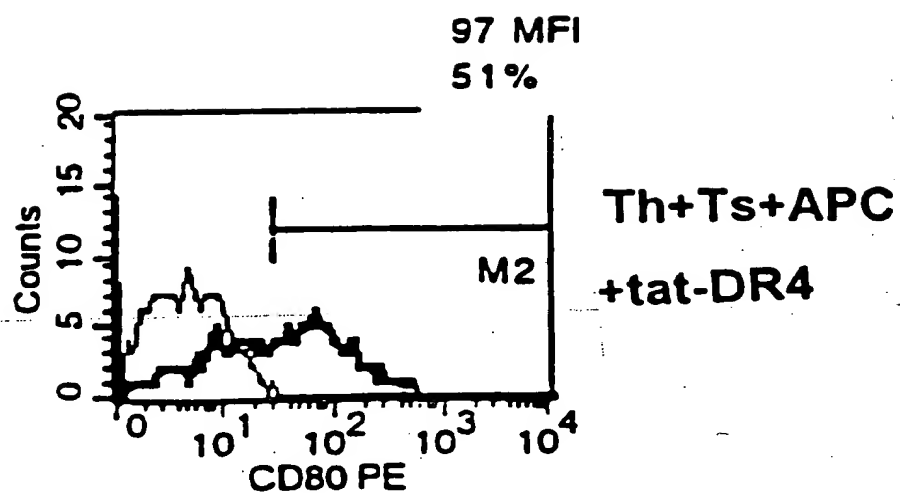


FIG. 20H

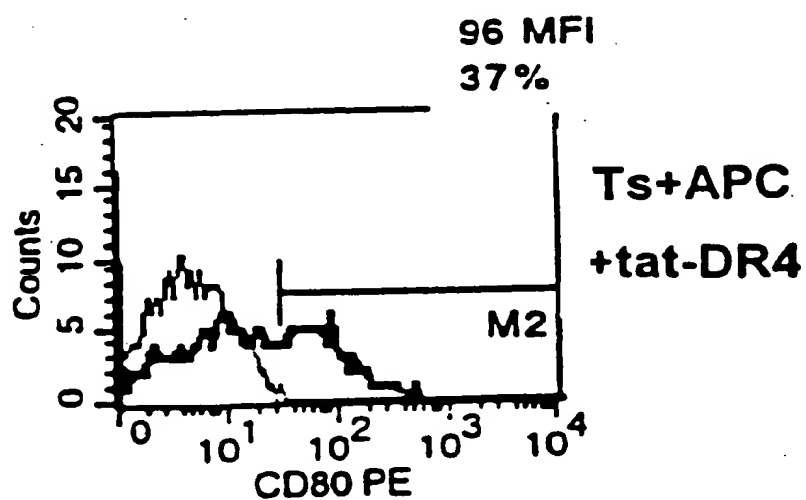




FIG. 20I

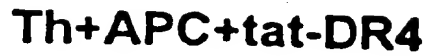


FIG. 20J

36/73

CD86

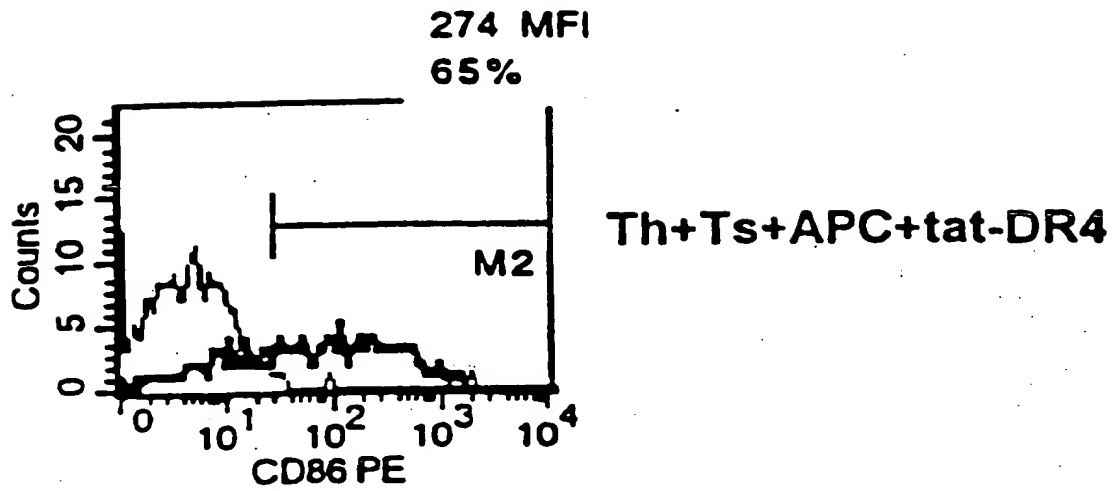


FIG. 20K

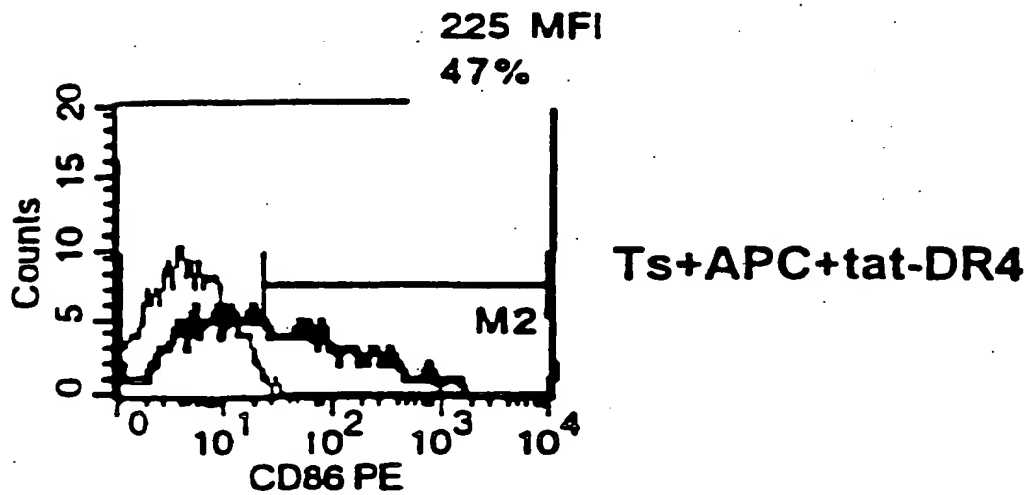


FIG. 20L

37/73

FIG. 21A

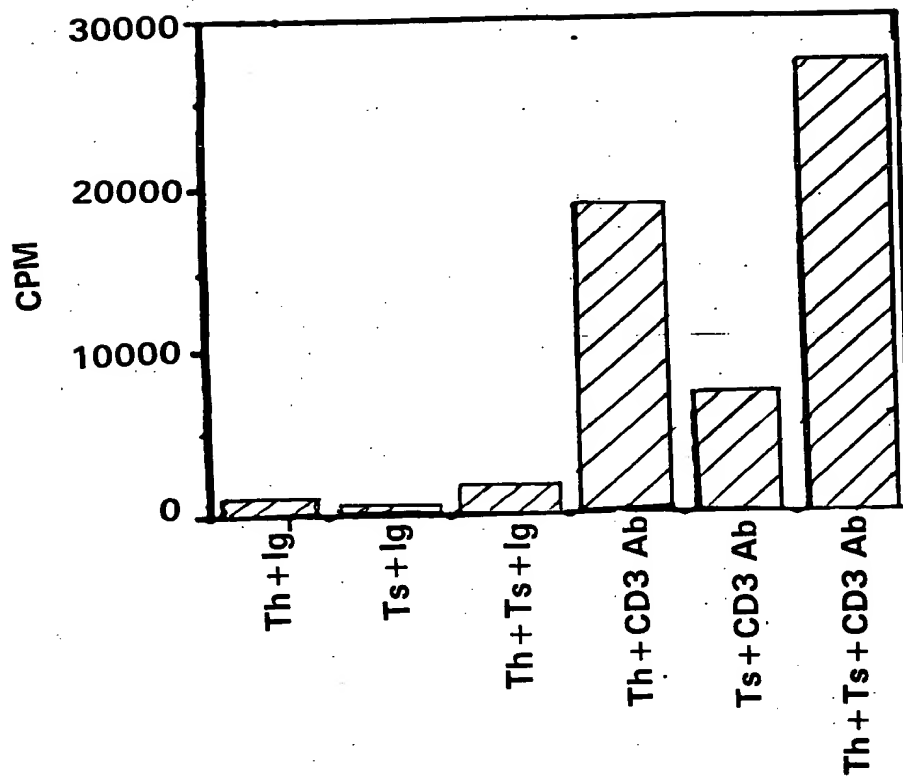
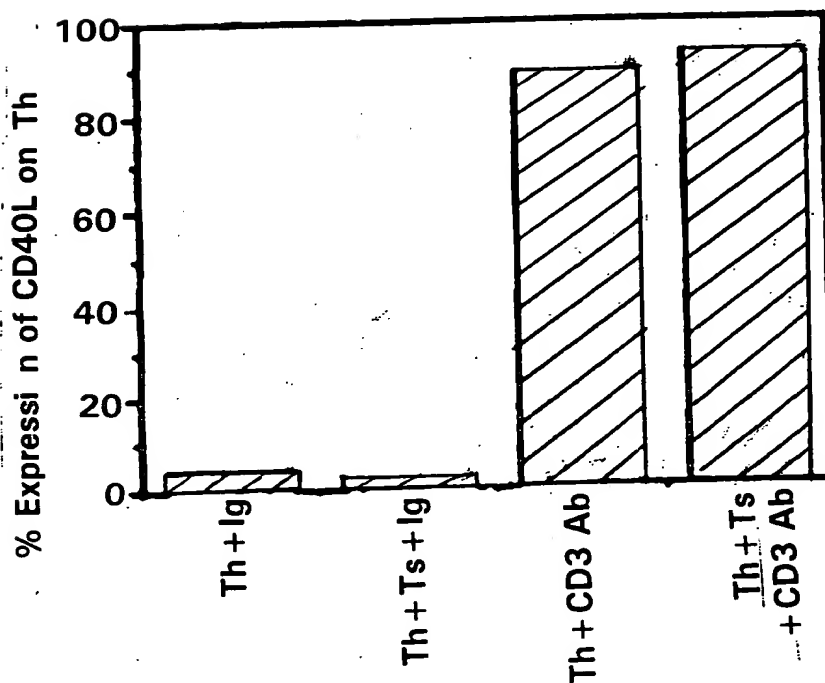


FIG. 21B



38/73

FIG. 21C

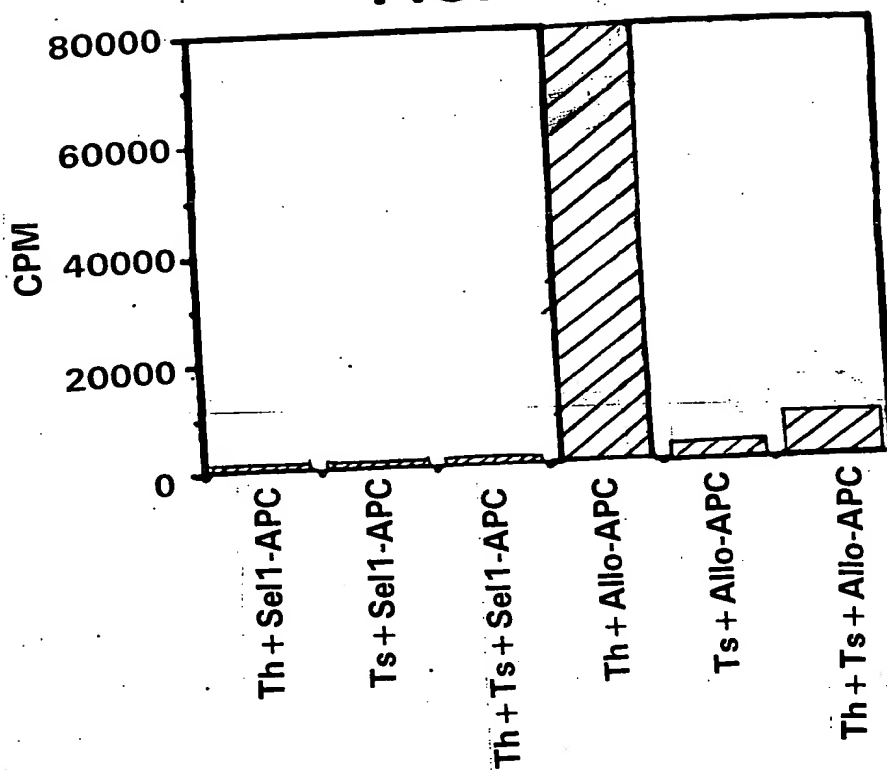
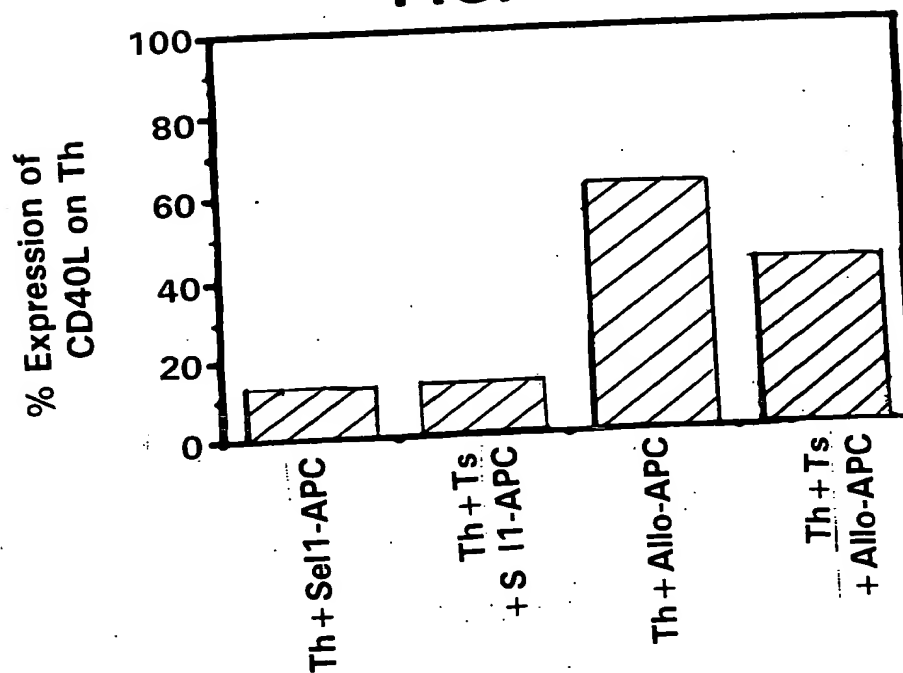
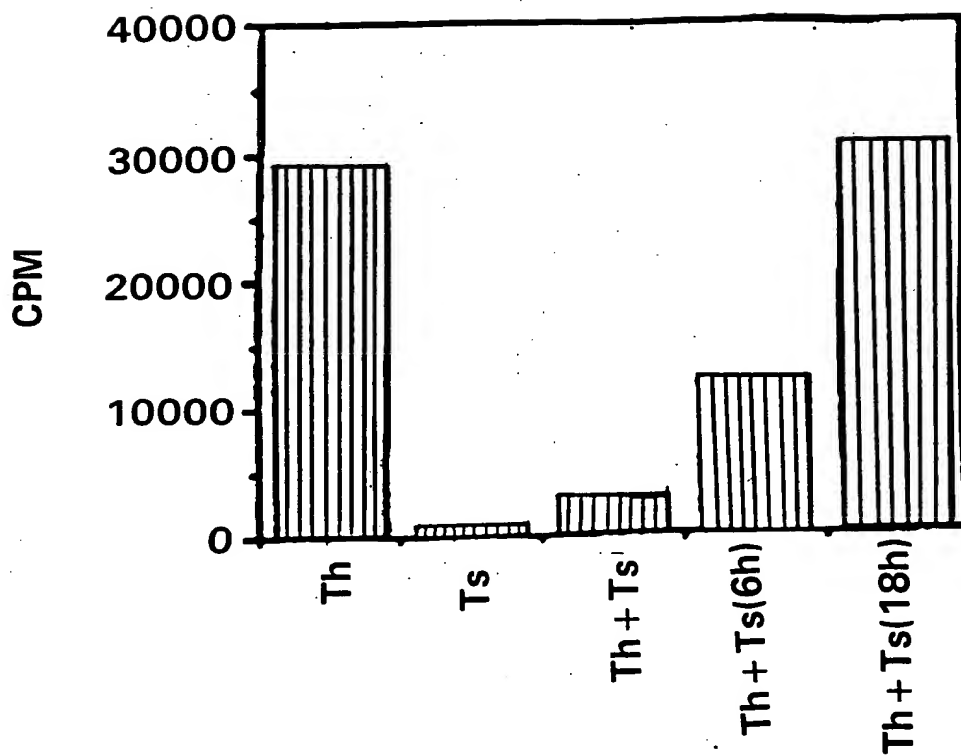


FIG. 21D

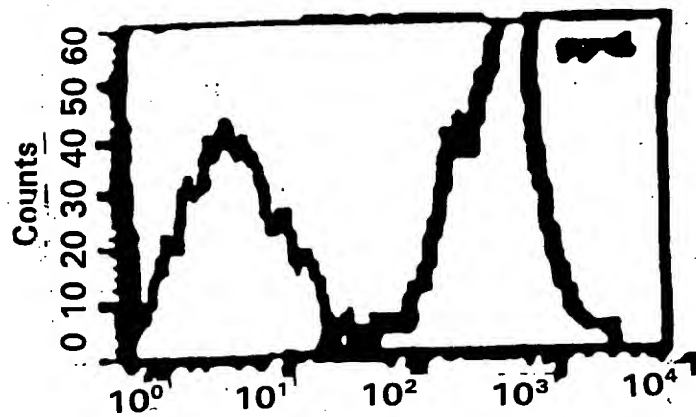
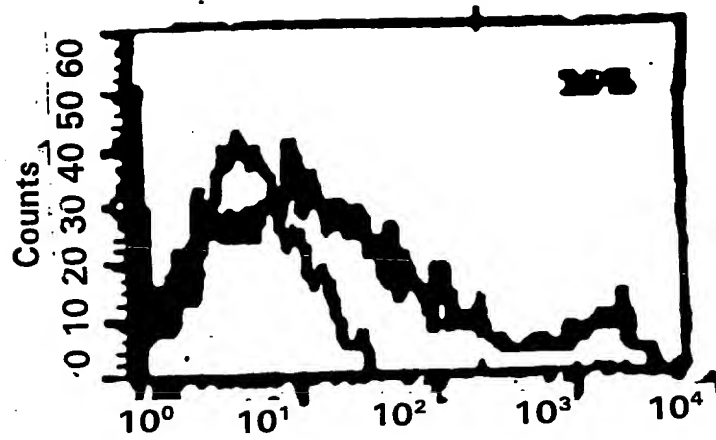


39/73

FIG. 22



Debt Relief



41/73

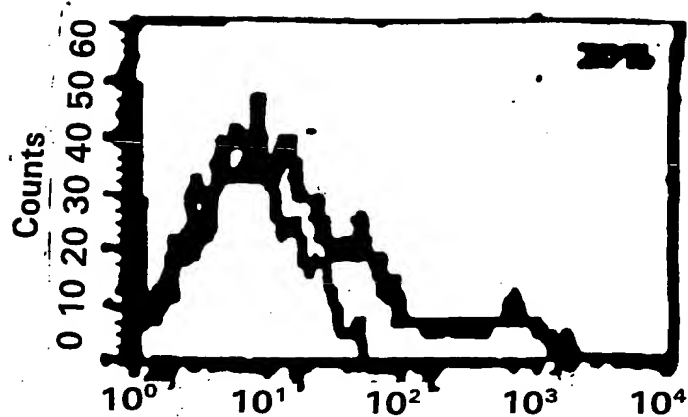


Fig. 23A-3
CD40

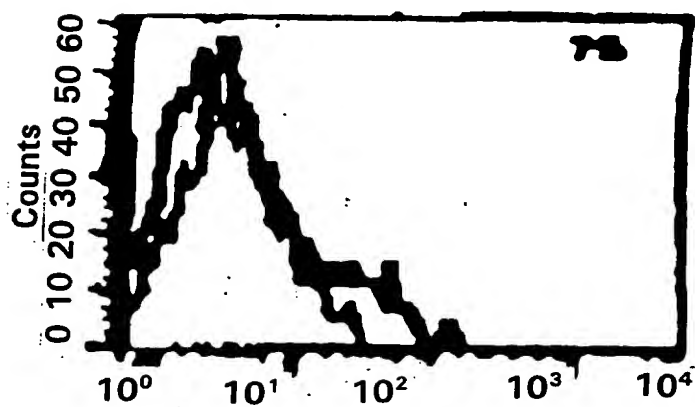


Fig. 23A-4
CD80

001221-11E94260

42/73

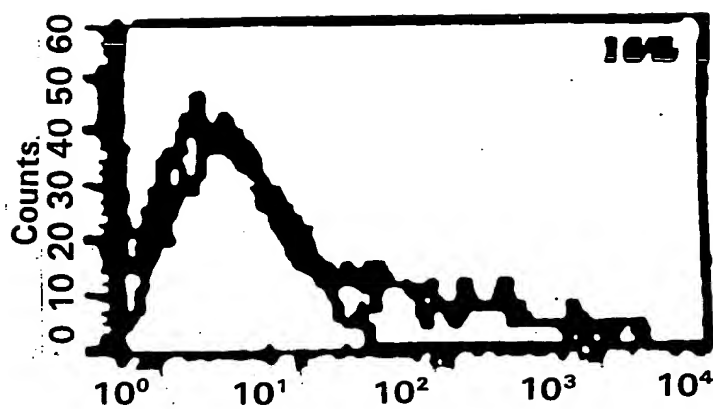


Fig. 23A-5
CD86

007227" TFE94260

43/73

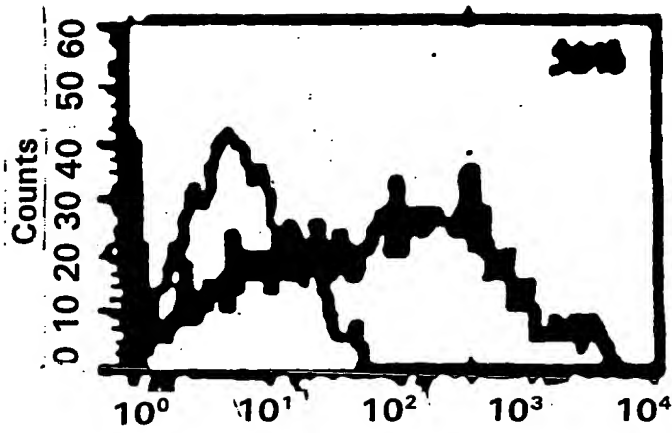


Fig. 23B-1
CD54

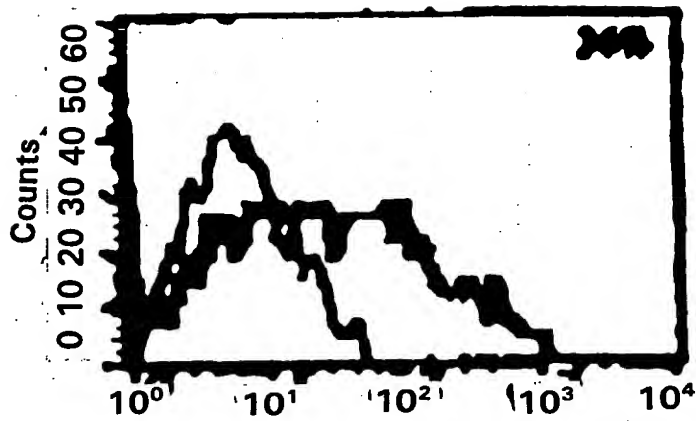


Fig. 23B-2
CD58

001221" T E 9 4 6 0

44/73

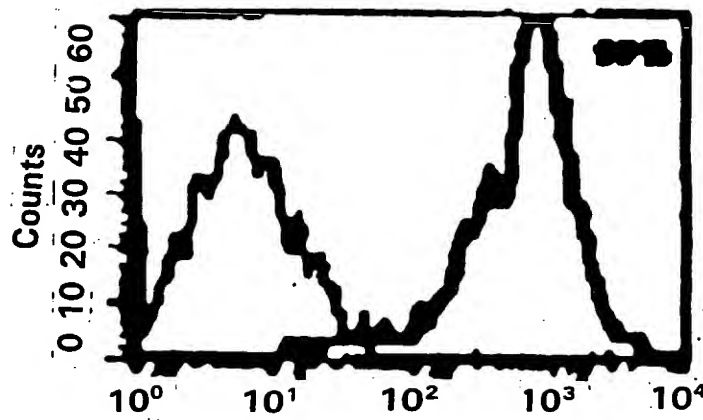


Fig. 23B-3
CD40

001221 1165460

45/73

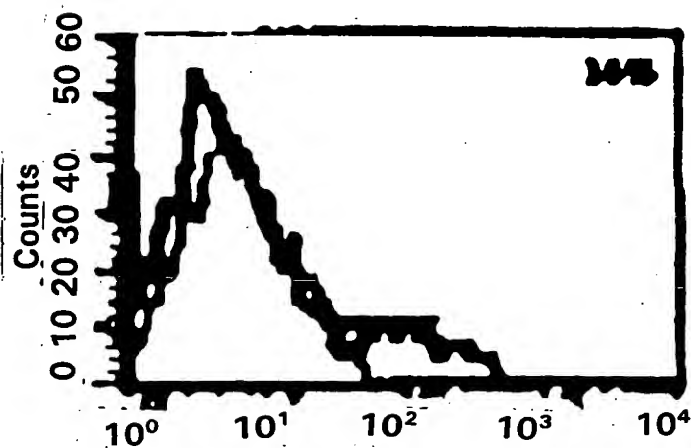


Fig. 23B-4
CD80

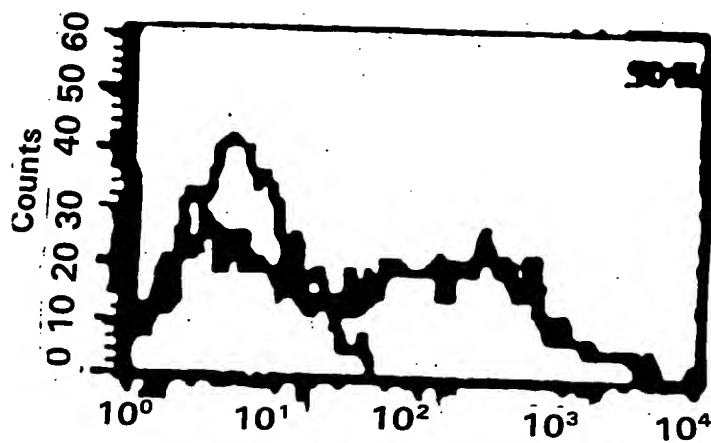
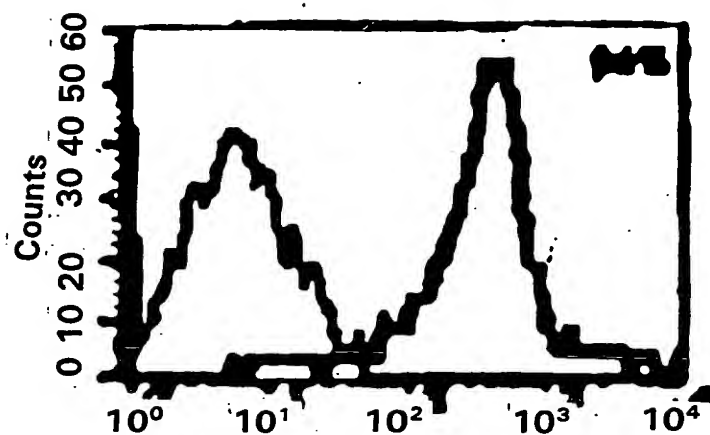
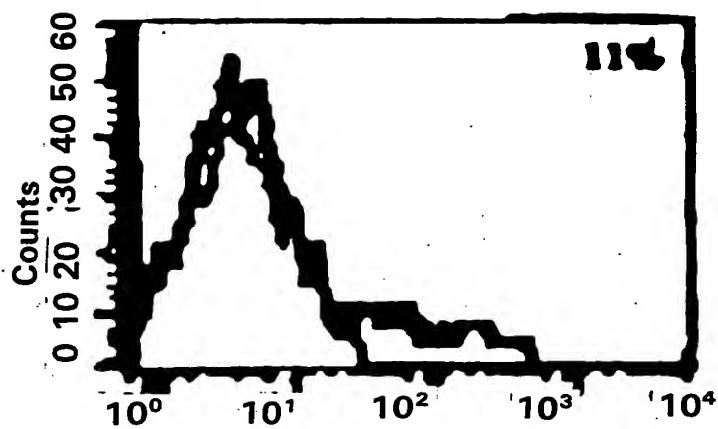
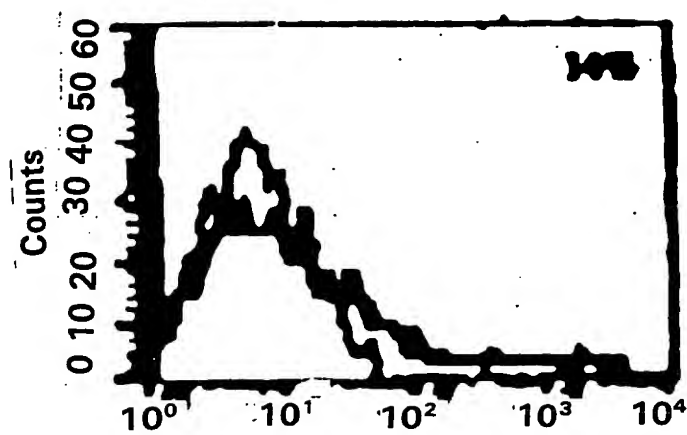


Fig. 23B-5
CD86

001231 1E94260



47/73

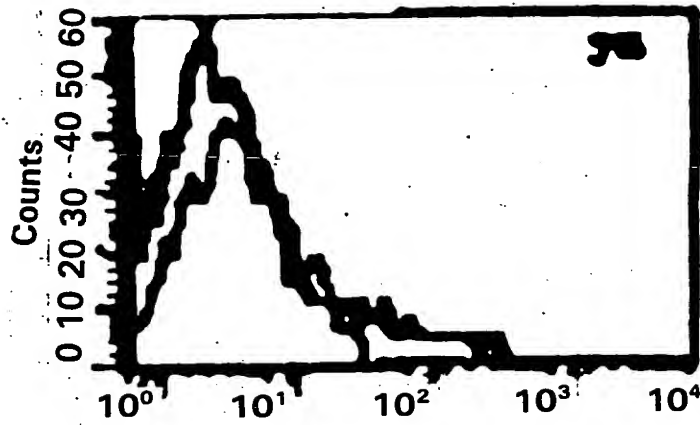


Fig. 23C-4
CD80

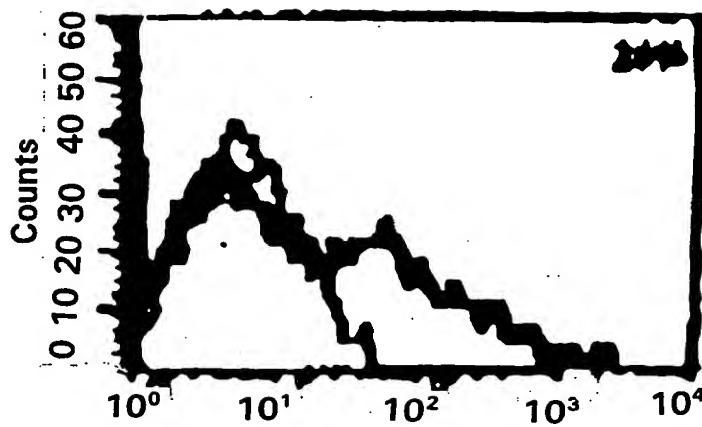


Fig. 23C-5
CD86

48/73

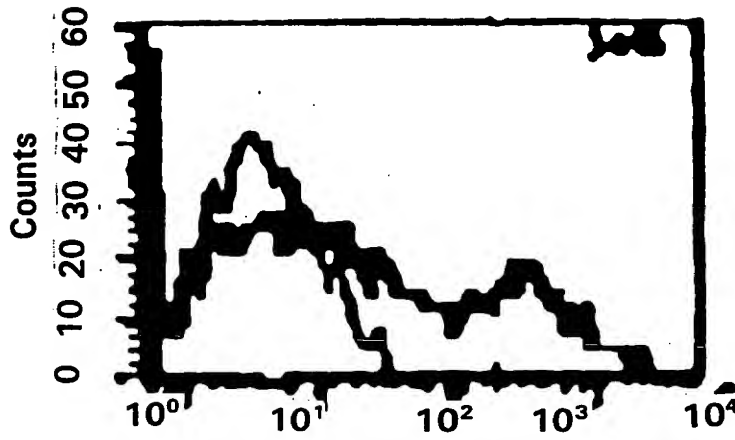


FIG. 23D-1
CD54

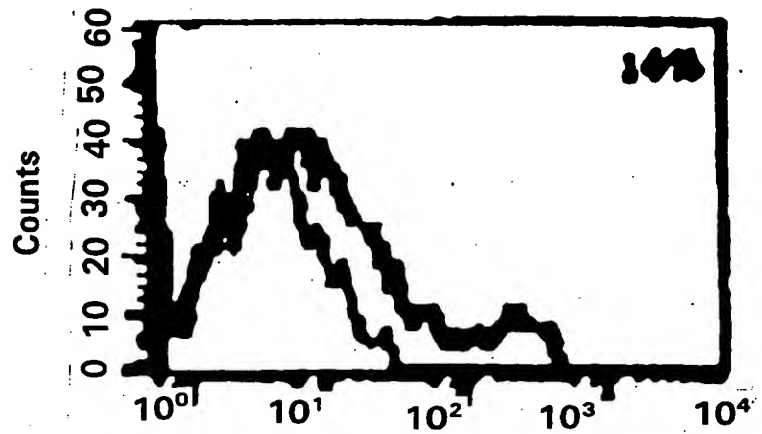


FIG. 23D-2
CD58

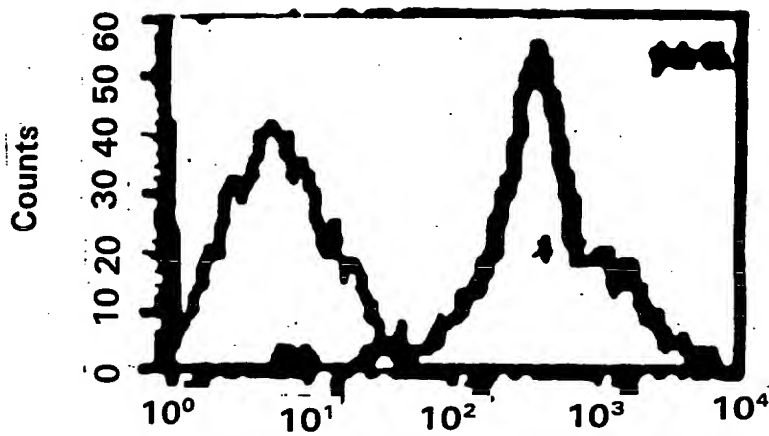


FIG. 23D-3
CD40

001221" TFE94260

49/73

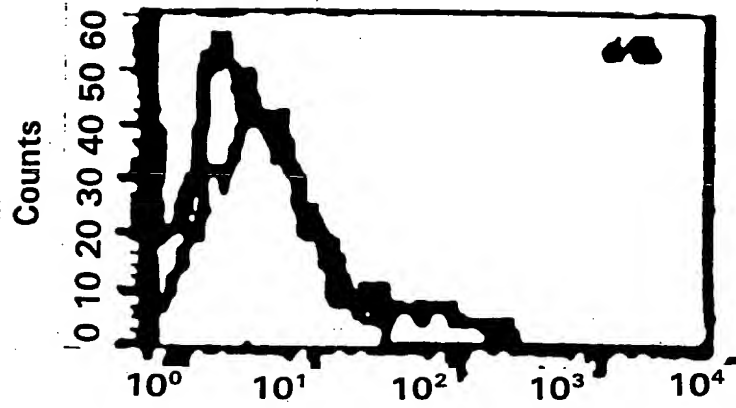


Fig. 23D-4
CD80

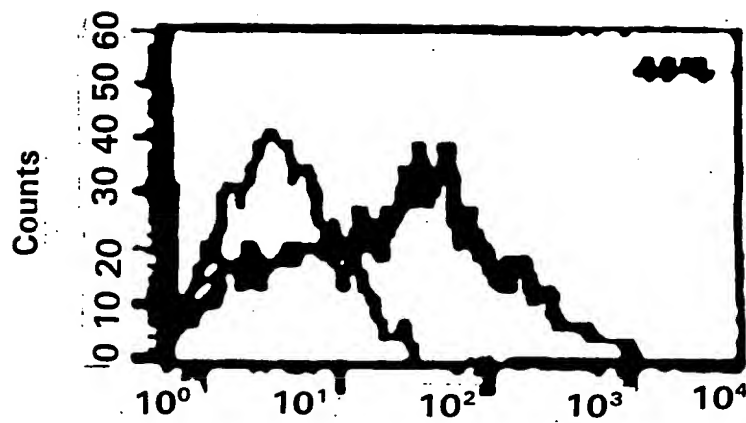


Fig. 23D-5
CD86

001221-11E94/60

50/73

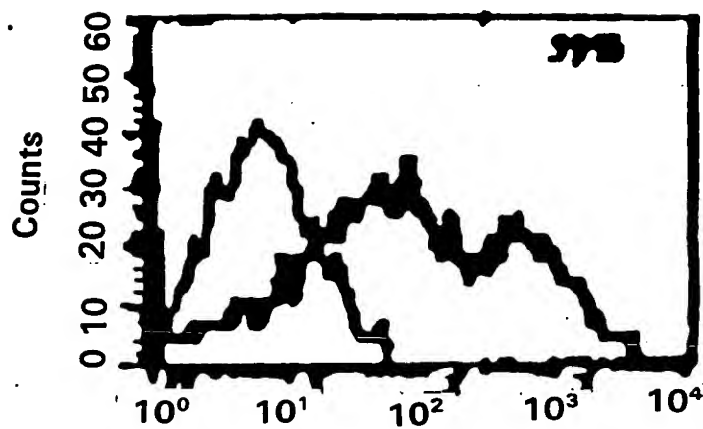


Fig. 23E-1
CD54

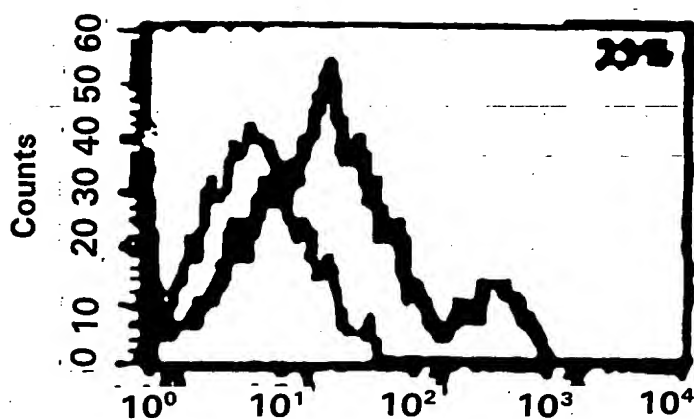


Fig. 23E-2
CD58

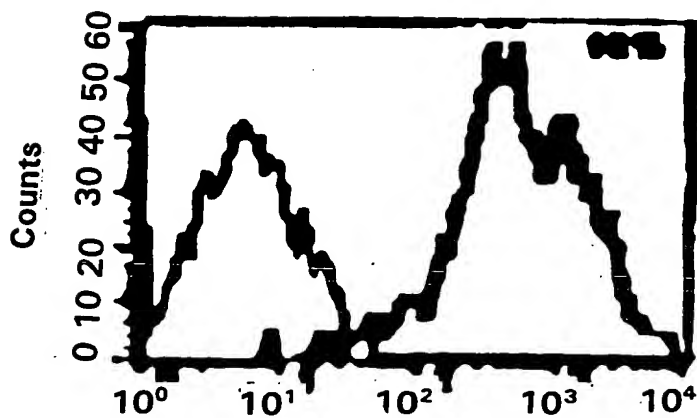


Fig. 23E-3
CD40

51/73

CD80

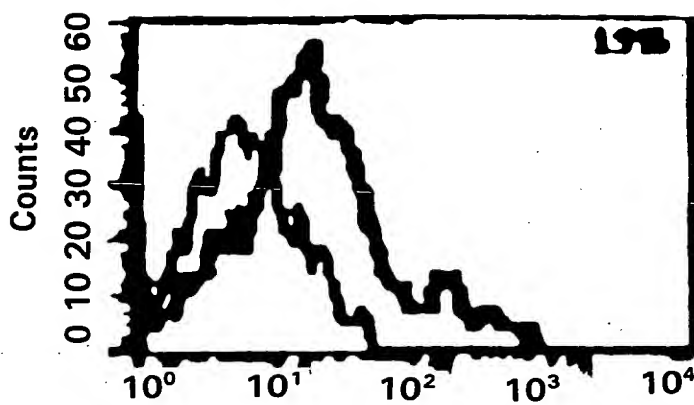


Fig. 23E-4

CD86

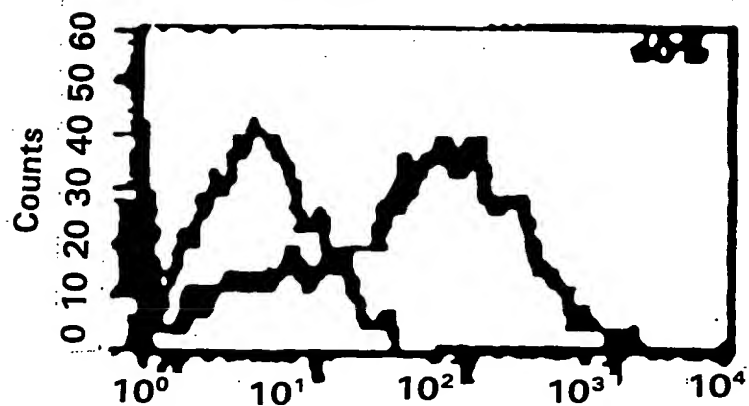
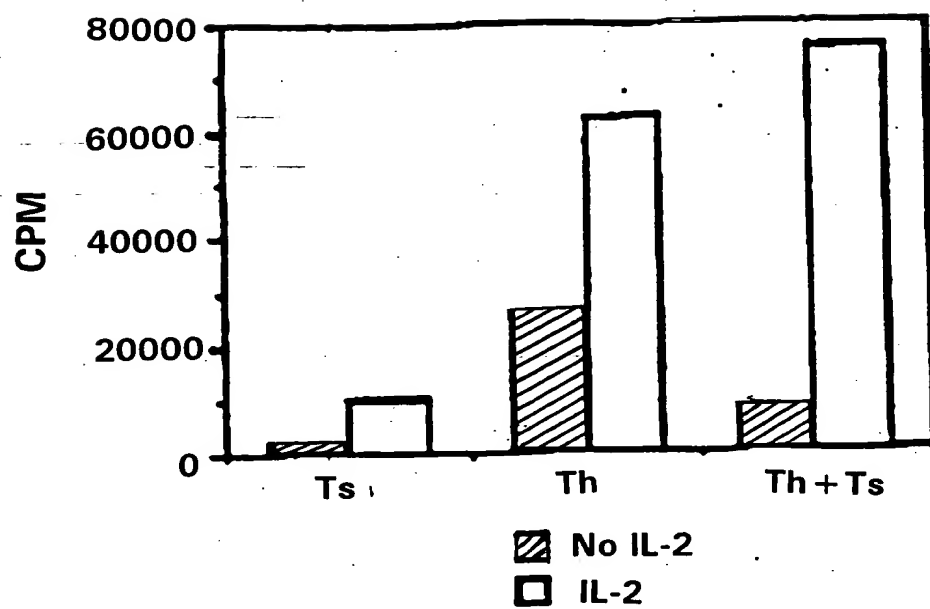


Fig. 23E-5

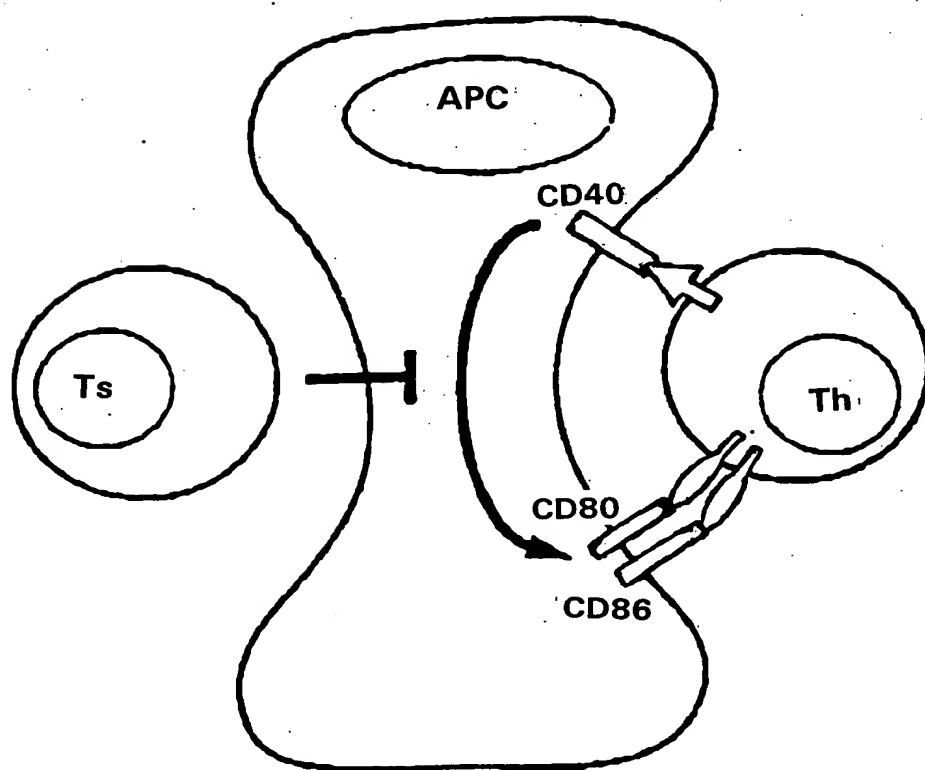
52/73

FIG. 24



53/73

FIG. 25



00746311-122100

54/73

FIG. 26

HLA A, B and DR Antigen Values and Split Equivalences

A Locus	Equivalent	B Locus	Equivalent	DR Locus	Equivalent
1	1	6	6	1	1
2	2	7	7	2	2,15,18
3	3	8	8	3	3,17,18
9	9	12	12	4	4
10	10,66	13	13	5	5,11,12
11	11	14	14,64,65	6	6,13,14
19	19,74	15	15,75,76,77	7	7
23	23	16	16	8	8
24	24	17	17,58	9	9
25	25	18	18	10	10
26	26	21	21	11	11,5
28	28,68,69	22	22,54,55,56	12	12,5
29	29	27	27	13	13,6
30	30	35	35	14	14,8
31	31	37	37	15	15,2
32	32	38	38	16	16,2
33	33	39	39	17	17,3
34	34	40	40,61	18	18,3
36	36	41	41	51	51
43	43	42	42	52	52
66	66,10	44	44	53	53
68	68,23	45	45	* 103	103
69	69,23	46	46	* 1403	1403
74	74,19	47	47	* 1404	1404
80	80	48	48	** 99	99
* 203	203	49	49		
* 210	210	50	50		
* 2403	2403	51	51		
** 99	99	52	52		
		53	53		
		54	54,22		
		55	55,22		
		56	56,22		
		57	57		
		58	58,17		
		59	59		
		60	60		
		61	61,40		
		62	62		
		63	63		
		64	64,14		
		65	65,14		
		67	67		
		70	70,71,72		
		71	71,70		
		72	72,70		
		73	73		
		75	75,15		
		76	76,15		
		77	77,15		
		* 703	703		
		* 3901	3901		
		* 3902	3902		
		* 4005	4005		
		* 5102	5102		
		* 5103	5103		
		* 7801	7801		
		* 8101	8101		
		** 99	99		

** Code 99 means not tested

001231-1-123100

55/73

FIG. 27A

DRB Protein Sequences - 20th March 1998 - SGE Marsh ANRI

10 20 30 40 50 60 70 80 90 100

DRB1*0101
 GDTRPRFLWQLKFECHFFNGTERVRLLERCIYNQEEVRFDSVGEYRAVTELGRPDAEYWNSQK
 DLLEQRRAAVDTYCRHNYGVGESFTVQRRVEPKVTYV
 DRB1*01021 _____AV_____
 DRB1*01022 *****
 AV*****
 DRB1*0103 _____I-DE_____
 DRB1*0104 _____N____V_____
 DRB1*15011 _____P-R____F-D-YF____F____I-A____V____Q____
 -
 DRB1*15012 *****P-R____F-D-YF____F____I-A____V____
 * *****
 DRB1*15021 _____P-R____F-D-YF____F____I-A____Q____
 -
 DRB1*15022 *****F-D-YF____F____I-A____

 DRB1*15023 *****P-R____F-D-YF____F____I-A____

 DRB1*1503 _____P-R____F-D-HF____F____I-A____V____Q____
 * *
 DRB1*1504 *****P-R____F-D-YF____F____F-A____V____

 DRB1*1505 *****P-R____F-D-YF____F____A____V____
 * *****
 DRB1*1506 *****P-R____F-D-YF____F-A____I-A____V____

 DRB1*16011 _____P-R____F-D-YF____F-D____Q____
 -
 DRB1*16012 *****P-R____F-D-YF____F-D____

 DRB1*16021 _____P-R____F-D-YF____D____Q____
 DRB1*16022 *****P-R____F-D-YF____D____

 DRB1*1603 _____P-R____F-D-YF____F-D-A____Q____
 -
 DRB1*1604 *****P-R____F-D-YF____F-D-L____
 * *****
 DRB1*1605 **** *P-R____F-D-YF____I-D____
 *** * *
 DRB1*1607 ***P-R____FPD-YF____I-D____
 **** *
 DRB1 1608 *****P-R____F-D-YF____N____F-D____
 * * * *
 DRB1*03011 _____EYSTS____Y-D-YFH____N____F____K-GR-N____V____
 -H____
 DRB1*03012 *****EYSTS____Y-D-YFH____N____F____K-GR-N____V____
 -*****

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56/73

FIG 27B

DRB1 03021 ———EYSTS———F—YFH—N———K-GR-N———
 H——
 DRB1*03022 ———EYSTS———F—YFH—N———K-GR-N———
 H——**
 DRB1*0303 *****YSTS———F—YFH—N———K-GR-N———V——
 —————
 DRB1*0304 *****EYSTS———Y-D-YFH———F———K-GR-N———V-
 ** *****
 DRB1*0305 *****EYSTS———Y-D-YFH—N———F———K-GR-N———
 —————
 DRB1*0306 *****EYSTS———Y-D-YFH—N———K-GR-N———V——
 .*****
 DRB1*0307 ———EYSTS———F-D-YFH—N———F———K-GR-N———V——
 -H——
 DRB1*0308 ———EYSTS———Y-D-YFH—N———F———E———K-GR-N———V——
 -H——
 DRB1*0309 *****EYSTS———Y-D-YFH-R-N———F———K-GR-N———
 —————
 DRB1*0310 ———EYSTS———Y-D-YFH—N———F———A-H———K-GR-N———V——
 —H——
 DRB1*0311 *****EYSTS———Y-D-YFH—N———F———K-GQ-N———V——
 —————
 DRB1*04011 ———E-V-H———F-D-YF-H—Y———K———Y-
 E——
 DRB1*04012 *****E-V-H———F-D-YF-H—Y———K———

 DRB1*0402 ———E-V-H———F-D-YF-H—Y———I-DE———V——
 * *****
 DRB1*0403 ———E-V-H———F-D-YF-H—Y———E———V———Y-
 E——
 DRB1*0404 ———E-V-H———F-D-YF-H—Y———V———Y-
 E——
 DRB1*04051 ———E-V-H———F-D-YF-H—Y———S———

 DRB1*04052 *****E-V-H———F-D-YF-H—Y———S———

 DRB1*0406 ———E-V-H———F-D-YF-H———E———V———Y-
 E——
 DRB1*0407 ———E-V-H———F-D-YF-H—Y———E———

 DRB1*0408 *****E-V-H———F-D-YF-H—Y———

 DRB1*0409 *** * ***———F-D-YF-H—Y———S———K———
 * *****
 DRB1 0410 * *** —E-V-H———F-D-YF-H—Y———S———V——
 * * *****
 DRB1 0411 ———E-V-H———F-D-YF-H—Y———S———E———V———Y-
 E——
 DRB1 0412 * —E-V-H———F-D-YF-H—Y———S———I-D-L———V——
 * *****
 DRB1 0413 * * * * *****H———F-D-YF-H—Y———K———V——

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FIG. 27C

DRB1 0415 *** *—E-V-H—F-D-YF-H—Y—E—F-D—V—
 ***** *
 DRB1*0416 *****—F-D-YF-H—Y—Q—K—

 DRB1*0417 *****—F-D-YF-H—Y—S—E—

 DRB1*0418 *****—F-D-YF-H—Y—I-D-L—V—
 * *****
 DRB1*0419 *****H—F-D-YF-H—

 DRB1*0420 *****—F-D-YF-H—E—
 * *****
 DRB1*0421 *****E-V-H—F-D-YF-H—K—

 DRB1*0422 *****E-V-H—F-D-YF-H—Y—K-GR-N—V—
 * *****
 DRB1*0423 *****—E-V-H—F-D-YF-H—Y—V-R—

 DRB1*0424 *****—E-V-H—F-D-YF-H—Y—S—R—

 DRB1*0425 *****E-V-H—F-D-YF-H—Y—F-D-L—V—

 DRB1*0426 *****—E-V-H—F-D-YF-H—Y—T—K—

 DRB1*0427 *****—E-V-H—F-D-YF-H—Y—E—AV—

 DRB1*11011 —EYSTS—F-D-YF—Y—F—E—F-D—
 H—
 DRB1*11012 —EYSTS—F-D-YF—Y—F—E—F-D—
 H—*
 DRB1*11013 *****EYSTS—F-D-YF—Y—F—E—F-D—

 DRB1*1102 —EYSTS—F-D-YF—Y—F—E—I-DE—V—
 H—
 DRB1*1103 —EYSTS—F-D-YF—Y—F—E—F-DE—V—
 H—
 DRB1*11041 —EYSTS—F-D-YF—Y—F—E—F-D—V—

 DRB1*11042 —EYSTS—F-D-YF—Y—F—E—F-D—V—
 H—
 DRB1*1105 *****EYSTG—F-D-YF—Y—F—E—F-D—

 DRB1*1106 *****EYSTS—F-D-YF—Y—F—E—F-D—AV—

 DRB1*1107 * *****EYSTS—F-D-YF—Y—F—E—K-GR-N—V—
 —*** *****
 DRB1 11081 *** *****S—F-D-YF—Y—F—E—D—
 ** * *
 DRB1*11082 ** * S—F-D-YF—Y—F—E—D—
 * * *****
 DRB1 1109 * * **—F-D-YFH—N—F—E—F-D—
 * * *
 DRB1 1110 ***** **—F-D-YFH—F—F—E—F-D—
 * *****

FIG. 27D

DRB1*1111 *** * * S — F-D-YF — Y — F — E — F-DE —

 DRB1*1112 ***** — F-D-YF — F — F — E — F-D —

 DRB1*1113 — EYSTS — F-D-YFH — F — F — E — R — V —
 * *****
 DRB1*1114 — EYSTS — F-D-YF — Y — F — E — I-DE —
 * *****
 DRB1*1115 — EYSTS — F-D-YF — DL — F — E — F-D —
 H —
 DRB1*1116 ***** — EYSTS — F-D-YFH — N — F — E — I-DE — V —
 .*****
 DRB1*1117 — EYSTS — F-D-YFH — F — E — R — E — V —
 H —
 DRB1*1118 ***** — EYSTS — F-D-YF — Y — F — E — I-D — V —

 DRB1*1119 ***** — EYSTS — F-D-YF — Y — F — E — I-D —

 DRB1*1120 ***** — EYSTS — F-D-YFH — N — F — E — I-DE —

 DRB1*1121 ***** — EYSTS — F-D-YF — Y — F — E — I-DE — AV —

 DRB1*1122 ***** — E-V-H — F-D-YF — Y — F — E — F-D —

 DRB1*1123 **** — EYSTS — F-D-YF — Y — F — E — F-D-L —

 DRB1*1124 ***** — EYSTS — F-D-YF — D — F — E — F-D —

 DRB1*1125 ***** — EYSTS — F-D-YF — Y — F — E — F-D-L — V —
 .*****
 DRB1*1126 ***** — EYSTS — F-D-YF — Y — F — E —

 DRB1*1127 ***** — EYSTS — F-D-YF — Y — F — E — F-D — N —

 DRB1*1128 ***** — EYSTS — F-D-YF — N — F — E — F-D —

 DRB1*1129 ***** — EYSTS — F-D-YF — F — E — F-D —

 DRB1*1130 ***** — EL-S — F-D-YF — Y — F — E — F-D —

 DRB1*1131 — EYSTS — F-D-YF — Y — F — E-H — I-D —
 H —
 DRB1*1201 — EYSTG-Y — HFH — LL — F — V-S — I-D — AV —
 -H —
 DRB1*12021 * ** — EYSTG-Y — HFH — LL — F — V-S — F-D —
 AV* * * * *
 DRB1*12022 * * — EYSTG-Y — HFH — LL — F — V-S — F-D — AV —
 * * * * *
 DRB1*12032 *** * — EYSTG-Y — HFH — LL — F — V-S — I-D — V —
 .* *****
 DRB1*1204 * ***** — EYSTG-Y — HFH — LL — F — E — I-D —
 AV * * * * *
 DRB1*1205 * * — EYSTG-Y — HFH — FL — F — V-S — I-D — AV —

Fig. 27E

DRB1*1301 —EYSTS—F-D-YFH—N—F—I-DE—V—
 H—
 DRB1*1302 —EYSTS—F-D-YFH—N—F—I-DE—
 H—
 DRB1*13031 —EYSTS—F-D-YF—Y—S—I-DK—
 H—*
 DRB1*13032 *****EYSTS—F-D-YF—Y—S—I-DK—

 DRB1*1304 —EYSTS—F-D-YF—Y—F—S—I-DE—V—
 H—*
 DRB1*1305 *****EYSTS—F-D-YFH—N—F—F-D—

 DRB1*1306 *****F-D-YFH—N—F—I-D—V—

 DRB1*13071 *****EYSTS—F-D-YF—Y—F-D—

 DRB1*1308 *****EYSTS—F-D-YFH—F—I-DE—V—

 DRB1*1309 *****EYSTS—F-D-YFH—N—F—I-A—V—

 DRB1*1310 *****EYSTS—F-D-YFH—N—F—I-DK—V—

 DRB1*1311 *****EYSTS—F-D-YF—Y—F—F-D—V—

 DRB1*1312 *****EYSTS—F-D-YF—Y—S—I-D—

 DRB1*1313 *****EYSTS—F-D-YF—Y—S—I-D-L—

 DRB1*1314 *****TS—F-D-YF—Y—F—F-D—

 DRB1*1315 *****EYSTS—F—YFH—N—F—I-DE—V—

 DRB1*1316 *****EYSTS—F-D-YFH—N—F—I-DE—D—

 DRB1*1317 —EYSTG—Y—F-D-YF—Y—F—I-DE—V—
 H—
 DRB1*1318 *****EYSTS—F-D-YFH—N—F—F-D-L—V—

 DRB1*1319 —EYSTS—F—YFH—F—I-DE—V—H—
 —
 DRB1*1320 *****EYSTS—F-D-YFH—N—F—DE—V—

 DRB1*1321 —EYSTS—F-D-YF—Y—F—S—F-D—H—
 —
 DRB1*1322 * **EYSTS—F-D-YF—Y—F—I-DE—V—
 ** ****
 DRB1*1323 ***EYSTS—F-D-YF—Y—F—I-DE—
 *** **
 DRB1*1324 * **EYSTS—F-D-YF—Y—F—F-DE—V—
 * ** *
 DRB1*1325 *****EYSTS—F-D-YF—Y—F—D—

 DRB1*1326 *****EYSTS—F—YFH—N—F-D—

60/73

Fig. 27F

DRB1 1327 * * * -EYSTS-----Y-D-YFH-N-----F-----I-DE-----V-----

 DRB1*1328 *****-EYSTS-----F-D-YFH-N-----F-----I-DE-----R-V-----
 * *****
 DRB1*1329 *****-EYSTS-----F-D-YFH-N-----F-----DE-----
 * *****
 DRB1*1330 *****-EYSTS-----F-D-YF-Y-----F-----S-----I-D-----

 DRB1*1331 *****-EYSTS-----F-D-YFH-N-----F-----V-----I-DE-----
 * *****
 DRB1*1332 *****-EYSTS-----F-D-YFH-N-----S-----I-DE-----V-----

 DRB1*1333 *****-EYSTS-----F-D-YF-Y-----S-----I-DK-N-----

 DRB1*1401 -----EYSTS-----F-D-YFH-F-----A-H-----R-E-----V-----
 * *****
 DRB1*1402 -----EYSTS-----F-YFH-N-----

 DRB1*1403 -----EYSTS-----F-YFH-N-----D-L-----

 DRB1*1404 *****-EYSTG-Y-----F-D-YFH-F-----A-H-----R-E-----V-----

 DRB1*1405 *****-EYSTS-Q-----F-D-YFH-F-----R-E-----V-----

 DRB1*1406 *****-EYSTS-----F-YFH-N-----V-----

 DRB1*1407 *****EYSTS-----F-D-YFH-F-----A-H-----R-E-----

 DRB1*1408 *****-EYSTS-----F-D-YFH-F-----H-----R-E-----V-----

 DRB1*1409 *****-EYSTS-----F-D-YFH-N-----

 DRB1*1410 *****-E-V-H-----F-D-YFH-F-----A-H-----R-E-----V-----

 DRB1*1411 *****EYSTG-Y-----F-D-YFH-F-----E-----R-E-----
 V*****
 DRB1*1412 *****S-----F-YFH-N-----D-L-----
 V*****
 DRB1*1413 *****EYSTS-----F-YFH-N-----S-----

 DRB1*1414 *****-EYSTS-----F-D-YFH-F-----R-E-----

 DRB1*1415 *****STG-Y-----F-D-YFH-F-----F-D-L-----V-----

 DRB1*1416 *****-EYSTS-----F-D-YFH-F-----A-H-----I-DE-----V-----
 ***** * * *
 DRB1*1417 * ** -EYSTS-----F-D-YFH-N-----F-----V-----
 * * * *
 DRB1*1418 ** **EYSTS-----F-YFH-N-----R-E-----V-----
 * * * *
 DRB1 1419 -----EYSTS-----F-YFH-N-----K-----
 ** * * *
 DRB1 1420 *****-EYSTS-----F-YFH-F-----V-----

09746311-122100

61/73

FIG. 27G

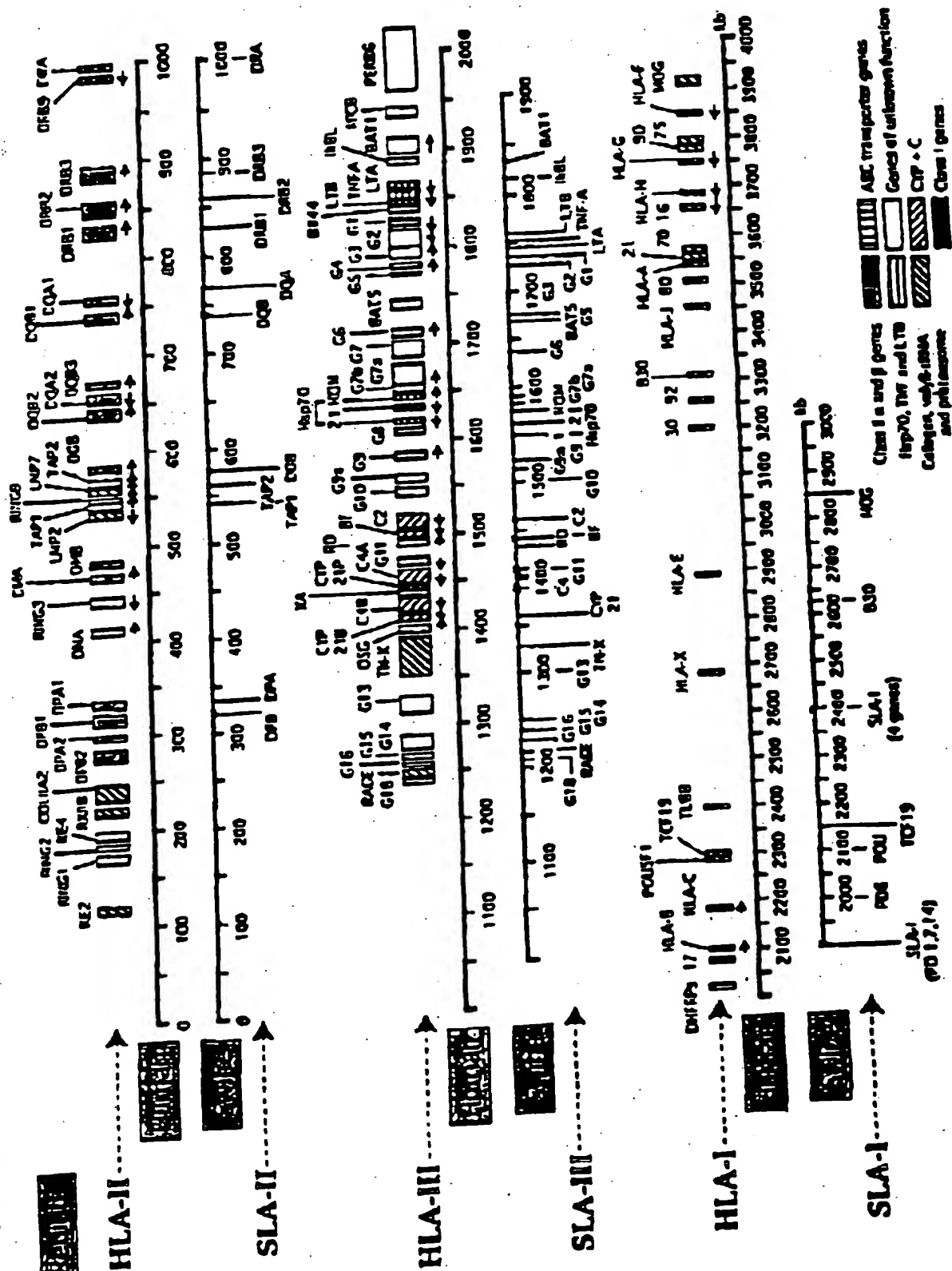
DRB1*1421 * ** -EYSTS—F-D-YFH—N—F—K—V—
 * * *
 DRB1*1422 *****-EYSTS—F-D-YFH—F—A-H—F-D—
 * * * * *
 DRB1*1423 *****-EYSTS—F-D-YFH—F—R-E—V—
 * * * * *
 DRB1*1424 *****-EYSTS—F—YFH—N—I—A—
 H—
 DRB1*1425 *****EYSTS—F-D-YF—Y—A-H—F-D—
 * * * * *
 DRB1*1426 *****-EYSTS—QF-D-YFH—F—A-H—R-E—V—
 - * * * * *
 DRB1*1427 *****-EYSTS—F—YFH—N—F-D—L—
 * * * * *
 DRB1*1428 *****-EYSTG—Y—F-D-YFH—F—A-H—R-E—
 AV * * * * *
 DRB1*1429 *****-EYSTS—F—YFH—N—AV—
 * * * * *
 DRB1*1430 *****-EYSTS—F-D-YFH—N—F—
 * * * * *
 DRB1*1431 *****-EYSTG—Y—F-D-YFH—F—A-H—R—V—
 * * * * *
 DRB1*0701 —Q—G-YK—QF—LF—F—V-S—I-D-GQ—V—
 H-E—
 DRB1*0703 *****-G-YK—QF—SLF—F—V-S—I-D-GQ—V—
 * * * * *
 DRB1*0801 —EYSTG—Y—F-D-YF—Y—S—F-D—L—
 * * * * *
 DRB1*08021 —EYSTG—Y—F-D-YF—Y—F-D—L—
 H—
 DRB1*08022 *****-EYSTG—Y—F-D-YF—Y—F-D—L—
 -H—
 DRB1*08032 —EYSTG—Y—F-D-YF—Y—S—I-D—L—
 H—
 DRB1*08041 —EYSTG—Y—F-D-YF—Y—F-D—L—V—
 H—*
 DRB1*08042 *****-F-D-YF—Y—F-D—L—V—
 . * * * * *
 DRB1*08043 *****-EYSTG—Y—F-D-YF—Y—F-D—L—V—
 . * * * * *
 DRB1*0805 *****-EYSTG—Y—F-D-YF—Y—S—F-D—
 * * * * *
 DRB1*0806 *****-EYSTG—Y—F-D-YF—Y—S—F-D—L—V—
 . * * * * *
 DRB1*0807 * ***-EYSTG—Y—F-D-YF—Y—V—F-D—L—
 * * * * *
 DRB1 0808 ** **EYSTG—Y—F-D-YF—Y—A-H—F-D—L—
 * * * * *
 DRB1*0809 * * * * *-Y—F-D-YFH—F—F-D—L—
 * * * * *
 DRB1*0810 * * *-EYSTG—Y—F-D-YF—Y—S—I-D—L—V—
 . * * *
 DRB1*0811 **** -EYSTG—Y—F-D-YF—Y—A—F-D—L—
 * * * * *

09746311-122100

FIG. 27H

DRB1*0812	*****-EYSTG-Y	F-D-YF-Y	S	I-D-L	AV
-----	*****				
DRB1*0813	*****-EYSTG-Y	F-D-YF-Y		D-L	
-----	*****				
DRB1*0814	*****-EYSRG-Y	F-D-YF-Y	S	I-D-L	
-----	*****				
DRB1*0815	*****-EYSTG-Y	F-D-YF-Y	H	I-D-L	
-----	*****				
DRB1*0816	*****-EYSTG-Y	F-D-YF-D	S	F-D-L	
-----	*****				
DRB1*0817	*****-EYSTG-Y	F-D-YF-Y	F	S	F-D-L
-----	*****				
DRB1*0818	*****-EYSTG-Y	F-D-YF-Y	S	I-D	
-----	*****				
DRB1*0819	*****-EYSTG-Y	F-D-YF-Y	I	I-D-L	
-----	*****				
DRB1*09012	Q-K-D	Y-H-G-N	V-S	F-R-E-V	
H-E					
DRB1*1001	EEV	RVH-YA-Y	R		Q

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64/73

FIG. 29

	1					50
Sladra-0102	-----	-----	-----	-----	-----	-----
Sladra-0202	-----	-----	-----	-----	-----	-----
Sladra-0203	-----	-----	-----	-----	-----	-----
Sladra-0101	-----	-----	-----	-----	-----	-----
Sladra-02011	-----	-----	-----	-----	-----	-----
Sladra-02012	-----	-----	-----	-----	-----	-----
Consensus	VENHVIIQAE	FYLSPDKSGE	FMFDFDGOEI	FHVDMEKRET	VWRLEEFQHF	
	51					100
Sladra-0102	-----	-----	-----	-----	-----	-----
Sladra-0202	-----	-----	-m-----	-----	-----	-----
Sladra-0203	-----	-----	-----	-----	-----	-----
Sladra-0101	-----	-----	-----	-----	-----	-----
Sladra-02011	-----	-----	-m-----	-----	-----	-----
Sladra-02012	-----	-----	-m-----	-----	-----	-----
Consensus	ASFEAQGALA	NIAVDKANLE	ILIKRSNNTF	NTNVPPEVTV	LSDKPVELGE	
	101					150
Sladra-0102	-----	-----	-----	-----	-----	-----
Sladra-0202	-----	-----	-----	-----	-----	-----
Sladra-0203	-----	-----	-----	-----	-----	-----
Sladra-0101	-----	-----	-----	-----	-----	-----
Sladra-02011	-----	-----	-----	-----	-----	-----
Sladra-02012	-----	-----	-----	-----	-----	-----
Consensus	PNILICFIDK	FSPPVVNVTV	LRNGSPVTRG	VSETVFLPRE	DHLFRKFHYL	
	151					200
Sladra-0102	-----	-----	-----	-r-----	-----	-----
Sladra-0202	-----	-----	-----	-----	-----	-----
Sladra-0203	-----	-----	-----	-----	-----	-----
Sladra-0101	-----	-----	-----	-----	-----	-----
Sladra-02011	-----	-----	-----	-----	-----	-----
Sladra-02012	-----	-----	-----	-----	-----	-----
Consensus	PFMPSTEDVY	DCQVEHWGLD	KPLLKHWEFE	AQTPLPETTE	NTVCALGLIV	
	201					228
Sladra-0102	-----	-----	-----	-----	-----	-----
Sladra-0202	-----	-----	---h---	-----	-----	-----
Sladra-0203	-----	-----	---h---	-----	-----	-----
Sladra-0101	-----	-----	-----	-----	-----	-----
Sladra-02011	-----	-----	-----	-----	-----	-----
Sladra-02012	-----	-----	-----	-----	-----	-----
Consensus	ALVGIIIVGTV	LIKGVKGN	ATERRGPL			

Group 01 has a leucine at residue 72 and Group 02 has a methionine.
No other polymorphisms have been found in the alpha 1 domain.

Amino Acid Sequences of SLA DRA Alleles

09745311.122100

65/73

FIG. 30

	1	2A	4A	50
Sladrb-T	--iaq--ffm	g-s-----	-----y-qky	l-----l--f--
Sladrb-N	-----f-	g-a-----	-----d-y	f--d-y--
Sladrb-M	-----f-	g-----	-----q-----	-----f-e-
Sladrb-Z	-----y-	-----	-----y-----	-----
Sladrb-AD	-----	-----	-----l-----	-----
Sladrb-C	--i-----q	-----	-----q-n	c-----y--
Sladrb-WX	-----	v-h--r----	-----l--d-y	f-----f--
Sladrb-Y	--i-----ffm	g-s-----	-----y-lky	l-----l--e-
Consensus	RDTPPHFLHL	LKFECHFFNG	TERVRLLEEQ	YNGEETFVRF
				DSDVGEYRAV
	51	6A	8A	100
Sladrb-T	-----	-----m--	k--v-----	-----
Sladrb-N	--f-----	-----fm--	k-----v--	-----e--e--
Sladrb-M	-----n	y-----	-----	-----ts--
Sladrb-Z	-----v-d	-----	-----	-----ts--
Sladrb-AD	-----d	-----	-----	-----
Sladrb-C	-----	r-----	-----a-----	-----
Sladrb-WX	-----	-----i--d	s--s-----i	-----
Sladrb-Y	-----	-----	-----ek-----	-----gvs-s--
Consensus	TELGRPDARY	WNSQKDLLEQ	RRAEVDITYCR	HNYRILDTEL
				VPRRAEPTVT
	101			150
Sladrb-T	-----	-----	-----	-----
Sladrb-N	-----	-----	-----	-----
Sladrb-M	-----	-----	-----	-----
Sladrb-Z	-----	-----	-----	-----
Sladrb-AD	-----	-----	-----	-----
Sladrb-C	-----	-----	-----	-----
Sladrb-WX	-----	-----	-----	-----
Sladrb-Y	-----	-----	-----	-----
Consensus	VYPAKTQPLQ	HHNLLVCSVT	GFYPGHVEVR	WFRNGQEEAA
				GVVSTGLIPN
	151			200
Sladrb-T	-----	-----	-----	-----
Sladrb-N	-----	-----	-----t-----	-----
Sladrb-M	-----	-----	-----	-----
Sladrb-Z	-----	-----	-----	-----
Sladrb-AD	-----	-----	-----	-----
Sladrb-C	-----	-----	-----	-----
Sladrb-WX	-----	-----	-----	-----
Sladrb-Y	-----	-----	-----	-----
Consensus	GDWTFQTMVM	LETVPQSGEV	YSCRVEHPSL	TSPVTVEWRA
				RSESAQGKMM
	201		237	
Sladrb-T	--v-----	-----	-----	-----
Sladrb-N	-----	-----	-----	-----
Sladrb-M	-----	-----	-----	-----
Sladrb-Z	--v-----	-----	-----	-----
Sladrb-AD	-----	-----	-----	-----
Sladrb-C	--v-----	-----	-----	-----
Sladrb-WX	-----	-----	-----	-----
Sladrb-Y	--v-----	-----	-----	-----
Consensus	SGIGGFVLGL	LFVAVGLFIY	FKNQKGRPAL	QPTGLLS

Amino Acid Sequence of SLA-DRB Alleles

00222111122400

66/73

FIG. 31

					50
Sladqa-02021	1	-----	-----	-----g	-----
Sladqa-02022		-----	-----	-----g	-----
Sladqa-02023		-----	-----	-----g	-----
Sladqa-0201		-----	-----	-----	-----
Sladqa-0101		-----	-r-----	---q-----	-----r---
Sladqa-0103		-----	-r-f-----	---q-----	-----r---
Sladqa-0102		-----	-----f-----	-----	-----r---
Consensus		EDIAADHVAS	YGLNVYQSYG	PSGYTTFEFD	GDEEFYVDLE KKETVWQLPL
					100
Sladqa-02021	51	---r-----	-----	-----	-----
Sladqa-02022		---r-----	-----	-----	-----
Sladqa-02023		---r-----	-----	-----	-----
Sladqa--201		-----	-----	-----	-----
Sladqa-0101		---e-----	-----1-	---vt-----	-----k---s---
Sladqa-0103		---e-----	-----1-	---vt-----	-----k---s---
Sladqa-0102		---e-----	-----1-	---vt-----	-----k---s---
Consensus		FSKFTSFDPQ	GALRNIATAK	HNLNILIKRS	NNTAAVNQVP EVTVFPKSPV
					150
Sladqa-02021	101	-----	-----	-----	-----
Sladqa-02022		-----	-----	-----	-----
Sladqa-02023		-----	-----	-----	-----
Sladqa-0201		-----	-----	-----	-----
Sladqa-0101		i-----	---s-----	-----	---k-----
Sladqa-0103		i-----	---s-----	-----	---k-----
Sladqa-0102		i-----	---s-----	-----	---k-----
Consensus		MLGQPNTLIC	HVDNIFPPVI	NITWLKNGHS	VTEGFSETSF LSKNDHSFLK
					200
Sladqa-02021	151	-----	-----	-----	-----
Sladqa-02022		-----	-----	-----	-----
Sladqa-02023		-----	-----	-----	-----
Sladqa-0201		-----	-----	-----	-----
Sladqa-0101		-----	-----	-----	-----
Sladqa-0103		-----	-----	-----	-----
Sladqa-0102		-----	-----	-----	-----
Consensus		ISYLTFLPSD	DDFYDCKVEH	WGLDKPLLKH	WEPEIPAPMS ELTETVVVAL
					232
Sladqa-02021	201	-----	-----	-----	---
Sladqa-02022		-----	-----	-----	---
Sladqa-02023		-----	-----	-----	---
Sladqa-0201		-----	-----	-----	---
Sladqa-0101		-----	-----	-----	---
Sladqa-0103		-----	-----	-----	---
Sladqa-0102		-----	-----	1-----	---
Consensus		GLIVGLVGIV	VGTVFIIQGL	RSGGPSRHQG	SL

Group 01 is 231 amino acids (deletion at 132) and Group 02 is 232 amino acids

Amino Acid Sequences of SLA-DQA Alleles

001221 " F E 3 4 2 5 0

67/73

FIG. 32

	1				50
Sladqb-D	-----v	---g---y-	-----ws-d	-----fl-	-----m-y-
Sladqb-D2	-----f	---g---y-	-----ws-d	-----fl-	-----m-y-
Sladqb-XA	-----	-----	-----g	wv-----	-----
Sladqb-Z	-----	-----y-	-----l-	wv--r-----	-----
Sladqb-W	-----	-----	-----l-t	-----ya-	-----y-
Sladqb-T	-----	-----	-----llt-	-----	-----n-y-
Sladqb-Y	-----	-----	-----h-t	-----	-----
Sladqb-C	-----f	---g---y-	-----g-	-----l-	-----
Consensus	GRDSPQDFVY	QFKFECYFFN	GTQVRV-VAR	YIYNQEEHVR	FDSDVGEFRA
	51				100
Sladqb-D	-----	-l---ea-	-----	-----	-----
Sladqb-D2	-----	-l---ea-	-----	-----	-----
Sladqb-XA	-----t-	-----	-----v-	-----	-----
Sladqb-Z	-----	-----e-	-----	-----	-----
Sladqb-W	-----a-	---s---i-	-t-----	-----	-----
Sladqb-T	-----	-----	-t-----	-----	-----
Sladqb-Y	-----	-----f-	-t-----	-----	-----
Sladqb-C	-----e-	s--s-----	-m--v-r-	-----	-----
Consensus	VTPLGRPDAD	YWNGQKDVLE	QKRAELDTVC	KHNYQIEEGT	TLQRRVQPTV
	101				150
Sladqb-D	-----	-----	-----	-----	-----
Sladqb-D2	-----	-----	-----	-----	-----
Sladqb-XA	-----	-----	-----	-----	-----
Sladqb-Z	-----	-----	-----	-----	-----
Sladqb-W	-----	-----	-----	-----	-----
Sladqb-T	-----	-----	-----	-----	-----
Sladqb-Y	-----	-----	-----	-----	-----
Sladqb-C	-----	-----	-----	-----	-----
Consensus	TISFSKAEAL	NHHNLLVCAV	TDFYPSQVKV	QWFRNGQEET	AGVVSTPLIR
	151				200
Sladqb-D	-----	-----	-----	-----	-----
Sladqb-D2	-----	-----	-----	-----	-----
Sladqb-XA	-----	-----	-----	-----n-----	-----
Sladqb-Z	-----	-----	-----	-----	-----
Sladqb-W	-----	-----	-----	-----	-----
Sladqb-T	-----	-----	-----	-----	-----
Sladqb-Y	-----	-----	-----	-----	-----
Sladqb-C	-----	-----	-----	-----n-----	-----
Consensus	NGDWTYQVLV	MLEMNLQRGD	VYTCRVEHSS	LQSPILVEWR	AQSESAQSKM
	201			230	
Sladqb-D	-----	-----	-----	-----	-----
Sladqb-D2	-----	-----	-----	-----	-----
Sladqb-XA	-----	-----	-----	-----	-----
Sladqb-Z	-----	-----	-----	-----	-----
Sladqb-W	-----	-----	-----	-----	-----
Sladqb-T	-----	-----	-----	-----	-----
Sladqb-Y	-----	-----	-----	-----	-----
Sladqb-C	-----	-----	-----	-----	-----
Consensus	LSGVGGFVLG	LIFLGLGLFI	RHRSQKGLVR		

Amino Acid Sequences of SLA-DQB Alleles

004431.123100

68/73

Figure 33

Nucleotide and Amino Acid Sequences of ILT3

1 atgatccccaccttcacggctctgctctgcctcgggctgagctctg
M I P T F T A L L C L G L S L
46 ggccccaggacccacatgcaggcagggcccctcccaaaccacc
G P R T H M Q A G P L P K P T
91 ctctgggctgagccaggctctgtgatcagctgggggaactctgtg
L W A E P G S V I S W G N S V
136 accatctggtgtcaggggaccctggaggctcgggagtaccgtctg
T I W C Q G T L E A R E Y R L
181 gataaagaggaaagcccagcaccctgggacagacagaacccactg
D K E E S P A P W D R Q N P L
226 gagcccaagaacaaggccagattctccatcccatccatgacagag
E P K N K A R F S I P S M T E
271 gactatgcaggagataccgctgttactatcgacccctgtaggc
D Y A G R Y R C Y Y R S P V G
316 tggtcacagcccagtgacccccctggagctggtgatgacaggagcc
W S Q P S D P L E L V M T G A
361 tacagtaaaccacccctttcagccctgccgagtcctctgtgacc
Y S K P T L S A L P S P L V T
406 tcaggaaagagcgtgaccctgctgtgtcagtcacggagcccaatg
S G K S V T L L C Q S R S P M
451 gacactttccttctgatcaaggagcgggacagcccatcccctactg
D T F L L I K E R A A H P L L
496 catctgagatcagagcacggagctcagcagcaccaggctgaattc
H L R S E H G A Q Q H Q A E F
541 cccatgagtcctgtgacctcagtgacggggggacctacaggtgc
P M S P V T S V H G G T Y R C
586 ttcagctcacacggcttctccactacctgctgtcacaccccagt
F S S H G F S H Y L L S H P S
631 gacccccctggagctcatagtctcaggatccttggagggtcccagg
D P L E L I V S G S L E G P R
676 ccctcacccacaaggctcgtctcaacagctgcaggccctgaggac
P S P T R S V S T A A G P E D
721 cagccccctcatgcctacagggtcagtcccccacagtggtctgaga
Q P L M P T G S V P H S G L R
766 aggcactgggaggtactgatcggggtcttgggtgtctccatcctg
R H W E V L I G V L V V S I L
811 cttctctccctcctctcttctcctcctccaacactggcgctcag
L L S L L L F L L L Q H W R Q
856 ggaaaaacacaggacattggcccagagacaggtgatttccaacgt
G K H R T L A Q R Q A D F Q R
901 cctccaggggctgccgagccagagcccaaggacgggggcctacag
P P G A A E P E P K D G G L Q
946 aggaggtccagcccagctgctgacgtccagggaagaaaacttctgt
R R S S P A A D V Q G E N F C
991 gctgccgtgaagaacacacagcctgaggacggggtggaaatggac
A A V K N T Q P E D G V E M D
1036 actcggagcccacacgatgaagacccccaggcagtgacgtatgcc
T R S P H D E D P Q A V T Y A
1081 aaggtgaaacactccagacctaggagagaaatggcctctcctccc
K V K H S R P R R E M A S P P
1126 tccccactgtctggggaattcctggacacaaaggacagacaggca
S P L S G E F L D T K D R Q A
1171 gaagaggacagacagatggacactgaggctgctgcatctgaagcc
E E D R Q M D T E A A A S E A
1216 ccccaggtgtgacctacgcccagctgcacagctttaccctcaga
P Q D V T Y A Q L H S F T L R
1261 cagaaggcaactgagcctcctccatcccaggaagggcctctcca
Q K A T E P P P S Q E G A S P
1306 gctgagcccagtgctctatgccactctggccatccactaa 1344
A E P S V Y A T L A I H *

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69/73

Figure 34A

Nucleotide and Amino Acid Sequences of *ILT4*

1 atgacccccatcgtcacagtcctgatctgtctcgggctgagtcctg
M T P I V T V L I C L G L S L
46 ggccccaggaccgcgtgcagacagggaccatccccaagcccacc
G P R T R V Q T G T I P K P T
91 ctgtgggctgagccagactctgtgatcaccaggggagtcctcgtc
L W A E P D S V I T Q G S P V
136 accctcagttgtcaggggagccttgaagcccaggagtaccgtcta
T L S C Q G S L E A Q E Y R L
181 tataggggagaaaaaatcagcatcttgattacacggatacagacca
Y R E K K S A S W I T R I R P
226 gagcttgtgaagaacggccagttccacatcccatccatcacctgg
E L V K N G Q F H I P S I T W
271 gaacacacagggcgatattggctgtcagttattacagccgcgctcgg
E H T G R Y G C Q Y Y S R A R
316 tggctctgagctcagtgacccccctgggtgctgggtgatgacaggagcc
W S E L S D P L V L V M T G A
361 tacccaaaacccaccctctcagcccagcccagccctgtgggtgacc
Y P K P T L S A Q P S P V V T
406 tcaggaggaagggtgaccctccagtggtgagtcacaggtggcattt
S G G R V T L Q C E S Q V A F
451 ggcggttctattctgtgtaaggaaggagaagatgaacacccacaa
G G F I L C K E G E D E H P Q
496 tgcctgaactcccagccccatgcccgtgggtcgtcccgcgccatc
C L N S Q P H A R G S S R A I
541 ttctccgtgggccccgtgagcccggaatcgaggtgggtcgacaggg
F S V G P V S P N R R W S H R
586 tgctatgggttatgacttgaactctccctatgtgtgggtcttcaccc
C Y G Y D L N S P Y V W S S P
631 agtgatctcctggagctcctgggtcccaggtgtttctaagaagcca
S D L L E L L V P G V S K K P
676 tcactctcagtgacgcccgtcctgtcatggcccctggggaaagc
S L S V Q P G P V M A P G E S
721 ctgaccctccagtggtgtctctgatgtcggtatgacagatttgtt
L T L Q C V S D V G Y D R F V
766 ctgtacaaggagggggaacgtgaccttcgccagctccctggccgg
L Y K E G E R D L R Q L P G R
811 cagccccaggctgggtctctccaggccaacttcaccctgggcccct
Q P Q A G L S Q A N F T L G P
856 gtgagccgctcctacgggggcccagtagatgctacgggtgcacac
V S R S Y G G Q Y R C Y G A H
901 aacctctcctctgagtgctcgccccccagcgacccccctggacatc
N L S S E C S A P S D P L D I
946 ctgatcacaggacagatccgtggcacacccttcattctcagtgacg
L I T G Q I R G T P F I S V Q
991 ccaggccccacagtggtcctcaggagagaacgtgaccctgctgtgt
P G P T V A S G E N V T L L C
1036 cagtcattggcggcagttccacactttccttctgaccaaggcgggga
Q S W R Q F H T F L L T K A G
1081 gcagctgatgccccactccgtctaagatcaatacagaatattcct
A A D A P L R L R S I H E Y P
1126 aagtaccaggctgaattcccatgagtcctgtgacctcagccac
K Y Q A E F P M S P V T S A H
1171 gcggggacctacaggtgctacgggtcactcaactccgacccctac
A G T Y R C Y G S L N S D P Y

09746344-122100

70/73

Figure 34B

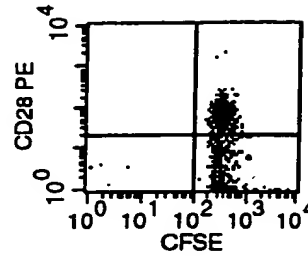
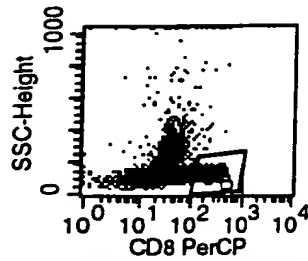
1216 ctgctgtctcaccacagtgagcccctggagctcgtgggtctcagga
L L S H P S E P L E L V V S G
1261 ccctccatgggttccagccccccaccacgggtcccatctccaca
P S M G S S P P P T G P I S T
1306 cctggccctgaggaccagcccctcacccccactgggtcggatccc
P G P E D Q P L T P T G S D P
1351 caaagtgggtctgggaaggcacctgggggttgatcggcattcttg
Q S G L G R H L G V V I G I L
1396 gtggccgtcgtcctactgctcctcctcctcctcctcctcctc
V A V V L L L L L L L L L F L
1441 atcctccgacatcgacgtcagggcaaactggacatcgacccag
I L R H R R Q G K H W T S T Q
1486 agaaaggctgatttccaacatcctgcaggggctgtggggccagag
R K A D F Q H P A G A V G P E
1531 cccacagacagaggcctgcagtggaggtccagcccagctgccgac
P T D R G L Q W R S S P A A D
1576 gcccaggaagaaaacctctatgctgccgtgaaggacacacagcct
A Q E E N L Y A A V K D T Q P
1621 gaagatggggtggagatggacactcgggctgctgcattctgaagcc
E D G V E M D T R A A A S E A
1666 ccccaggatgtgacctacgcccagctgcacagcttgaccctcaga
P Q D V T Y A Q L H S L T L R
1711 cggaaggcaactgagcctcctccatcccaggaaagggaacctcca
R K A T E P P P S Q E R E P P
1756 gctgagcccagcatctacgccaccctggccatccactag 1794
A E P S I Y A T L A I H *

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71/73

Figure 35

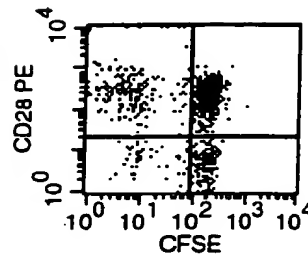
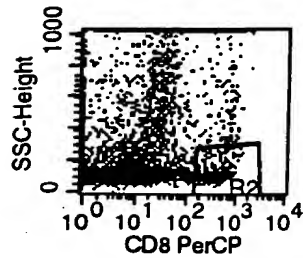
DAY 0



Gate: G1

Quad	Events	% Gated	X M	an
UL	0	0.00		***
UR	439	56.79	350.95	
LL	4	0.52	2.80	
LR	330	42.69	482.99	

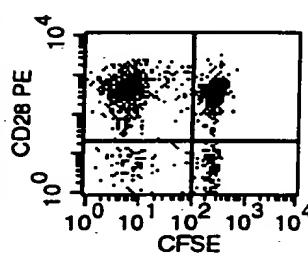
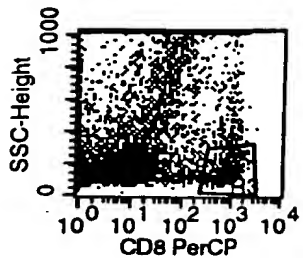
DAY 5



Gate: G2

Quad	Events	% Gated	X Mean
UL	214	13.70	14.01
UR	1134	72.60	202.84
LL	45	2.88	26.18
LR	169	10.82	190.79

DAY 7



Gate: G3

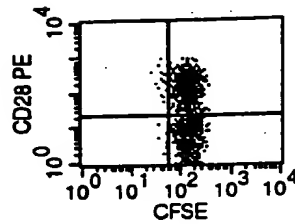
Quad	Events	% Gated	X Mean
UL	2290	38.33	9.23
UR	2973	49.77	273.42
LL	261	4.37	12.50
LR	450	7.53	242.13

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72/73

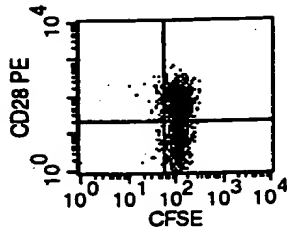
Figure 36

0 HR



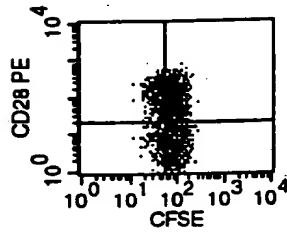
Quad	Events	% Gated	X Mean
UL	18	1.36	40.96
UR	737	55.62	143.24
LL	10	0.75	47.01
LR	560	42.28	151.29

48 HR
+APC



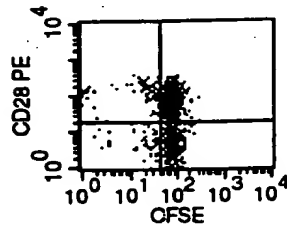
Quad	Events	% Gated	X Mean
UL	53	2.86	42.38
UR	1212	65.48	122.49
LL	23	1.24	41.38
LR	563	30.42	121.41

48 HR
+APC+IL2



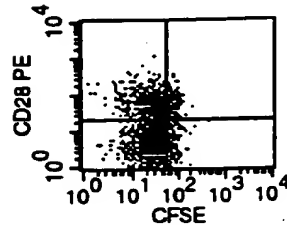
Quad	Events	% Gated	X Mean
UL	645	19.00	39.93
UR	1382	40.72	95.07
LL	311	9.16	40.05
LR	1056	31.11	101.61

72 HR
+APC



Quad	Events	% Gated	X Mean
UL	114	9.19	27.62
UR	711	57.34	78.27
LL	57	4.60	24.32
LR	358	28.87	83.25

72 HR
+APC+IL2

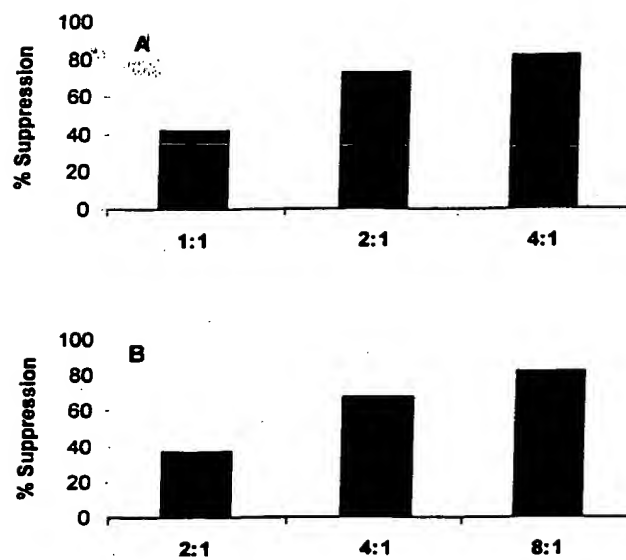


Quad	Events	% Gated	X Mean
UL	2911	30.97	28.62
UR	717	7.63	76.38
LL	4965	52.83	29.50
LR	805	8.57	74.95

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73/73

Figure 37



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